GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein August 25, 2005, 09:19:57 e ::

; Search time 23 Seconds (without alignments) 1087.280 Million cell updates/sec

US-10-724-972A-6352 1690 Perfect score:

1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

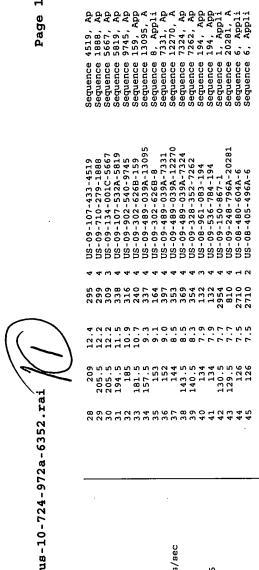
Database

Issued Patents AA:\*

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* ........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1 405 24.0 330 4 US-09-B30-217-16 2 405 24.0 330 4 US-09-B30-217-16 3 405 24.0 330 4 US-09-B30-217-16 5 307.5 18.2 330 4 US-10-278-946-15 6 296.5 17.5 351 3 US-09-107-532A-4516 8 292 17.3 347 4 US-09-134-001C-5492 8 292 17.3 347 4 US-09-710-279-462 9 293 16.7 317 4 US-09-710-279-462 10 283 16.7 317 4 US-09-710-279-462 11 283 16.7 317 4 US-09-710-279-462 12 28 16.5 325 4 US-09-710-279-462 13 266 15.7 30 4 US-09-134-001C-4860 14 266 15.7 36 4 US-09-134-001C-4860 15 26 15.7 36 4 US-09-134-010-3986 16 254 15.0 344 4 US-09-543-6444 17 250 14.8 325 4 US-09-583-110-373 18 240 14.2 312 4 US-09-583-110-373 18 240 14.2 312 4 US-09-38-35-4444 18 25 14.0 298 4 US-09-134-000C-6014 28 28 28 13.5 28 4 US-09-017-33-480 29 29 14.0 298 4 US-09-583-12 20 20 14.8 325 4 US-09-138-444 21 240 14.2 312 4 US-09-138-35-7 22 236 14.0 298 4 US-09-134-000C-6014 24 25 12 12 12 8 12 4 US-09-58-12 25 228 13.5 289 4 US-09-01-035-7 26 286 286 286 286-12 27 21 12.8 321 4 US-09-01-035-7 28 286 29-302-626-12 28 29 13.5 289 4 US-09-01-035-7 29 29 13.5 289 4 US-09-01-035-7 20 21 12.8 321 4 US-09-302-626-12 28 22 23 4 US-09-302-626-12 29 20 20 20 20 20 20 20 20 20 20 20 20 20	Result No.	Score	& Query Match	Length	DB	SUMMAKIES	Description
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292 17.3 347 4 US-09-710-279-1268 283 16.7 317 4 US-09-710-279-1268 284 16.7 327 4 US-09-710-35-38 278.5 16.5 325 4 US-09-643-681A-5565 268 15.9 296 4 US-09-543-681A-5565 265 15.7 60 3 US-09-134-001C-4860 254 15.0 306 4 US-09-662-787A-572 254 15.0 344 4 US-09-134-001C-4860 250 14.8 325 4 US-09-134-001C-4860 250 14.8 325 4 US-09-134-001C-2973 240 14.6 332 4 US-09-107-433-489 241 14.3 324 4 US-09-107-433-444 240 14.2 312 4 US-09-071-035-70 236 14.0 298 3 US-09-071-035-70 236 14.0 298 4 US-09-071-035-72 236 14.0 301 4 US-09-134-000C-6014 236 13.5 289 4 US-09-071-035-72 218 12.9 321 4 US-09-071-035-72 217 12.9 321 4 US-09-0302-6268-12	8	292	17.3	347	4	-60	
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236 14.0 298 4 US-09-536-784-24 236 14.0 301 4 US-09-134-000C-6014 228 13.5 289 4 US-09-071-035-72 218 12.9 321 4 US-09-302-626B-12 217 12.8 321 4 US-09-302-626B-10	22	236	14.0		ო	-08-961-083-2	
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217 12.8 321 4 US-09-302-626B-10	26	218		321	4	-09-302-626B-1	12,
	27	217	12.8	321	4	-09-302-626B-1	10,



## ALIGNMENTS

eus Genes and Polypeptides 217 99	05; DB 4; Length 330; c. 1.9e-25; atches 132; Indels 34; Gaps 12; SKESSKGGVEIKHEGTTKVPKHPKRVVVLEYS 67
RESULT 1  US-09-830-217-16  Sequence 16, Application US/09830217  Patent No. 6521441  GENERAL INFORMATION:  APPLICANT: Human Genome Sciences, Inc.  TITLE OF INVENTION Staphylococcus aureus Genes FILE REFERENCE: PB461PCT  CURRENT APPLICATION NUMBER: US/09/830,217  CURRENT APPLICATION NUMBER: PCT/US99/06199  PRIOR FILING DATE: 1999-03-18  PRIOR FILING DATE: 1998-04-01  PRIOR FILING DATE: 1998-05-07  PRIOR FILING DATE: 1998-05-07  PRIOR FILING DATE: 1998-05-07  SOFFWARE: Patentin Ver. 2.0  SEQ ID NO 16  LENGTH: 330  LENGTH: 330  TYPE: PRT  CURRANISM: Staphylococcus aureus  US-09-830-217-16	Query Match Best Local Similarity 32.8%; Pred. No. 1.9e-25; Best Local Similarity 32.8%; Pred. No. 1.9e-25; Matches 113; Conservative 65; Mismatches 132; Indels 34; Gaps  8 LKILSVIGLLFVLIATAACGNNSSNSSKESSKÖGVEIKHEEGTTKVPKHPKRVVVLEYS  8 IKILSVIGLLFVLIATAACGNNSSNSSKESSKÖGVEIKHEEGTTKVPKHPKRVVVLEYS  8 IKILSVIGLLFVLIATAACGNNSKSNSSKESSKÖGVEIKHEEGTTKVPKHPKRVVVLEYG  68 FVDALVALDVKPVGIADDNKKNRIIKPLRNCIGKYTSVGTRKOPNLEBISKLKPDLIIAD  63 ATDVANSLGVKPVGANESMTÖKPKERYIKNDLKDTKIVGQEDAPNLEBISKLKPDLIIAS  128 NNPHKGIYKOLNKIAPTIELKSFPGDYNBNIDAFKTISKALGKEEEGKRELEEHDKKIEE  128 NNPHKGIYKOLNKIAPTIELKSFPGDYNBNIDAFKTISKALGKEEEGKRELEEHDKKIEE  129 KVRNEKVYDQLSKIAPTVSTDTVFKFK-DTTKLMGKALGKEKEAEDLLKKYDDKVAA  188 YKKEITMDKNQKVLDAAAKSGLLAHPSNSYVGGFLSGLGFKEALSDDVTKGL  179 FQKDAKAKYKDAMPLKASVVNFRADHTRIYAGGYAGEILNDLGFKRNKDL  241 SKYLKGPYLQMMT-ETLSQVNPFRADHTRIYAGGYAGEILNDLGFKRNKDL  229 QKQVDNGKDIIQLTSKESIPLMNADHIFVVKSDPNAKDAALVKKTESEWTSSKEWKNLDA
RESULT US-09- Seque Seque GENE APP TILL CUR CUR PRI PRI PRI PRI PRI PRI PRI PRI PRI PR	

293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335

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63 ATDVAVSLGVKPVGAVESWTQKPKFRYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
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Patent No. 6737248
GENERAL INFORMATION
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34;
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1.9e-25;
                                                                                                                                                                                           289 VKANQVSDDLDEITWALAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.0%; Score 405; 32.8%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATFLLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TOTEL STATEMENT ON THE STATEMENT OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRRSSEE: Human Genome Scie
STREET: 9410 Key West Avenue
CITY: Rockville
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-781-986A-5193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-781-986A-5193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850
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Best Local
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                                ò
                                                                                                                                                                                                                                                                                                                   Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTURES: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IKML-VVTLAFILV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
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32.8%; Pred. No. 1.9e-25;
tive 65; Mismatches 132; Indels
289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
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APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTONNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
RESPERCEC, DOCKET NUMBER: P8248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-OCt-1997
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SEQUENCE DESCRIPTION: SEQ ID NO: 5193:
                                                                                                                                                 Sequence 5193, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                             Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.81
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                       US-08-956-171E-5193
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Best Local S
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Sequence 4516, Application US/09107532A
Patent No. 6581275
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKYLKG--PYLOMNT-ETLSOVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Simpson et al.
TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REFERENCE: P8461USDI;
CURRENT APPLICATION NUMBER: US/10/278,946
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/830,217
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 60/080,296
PRIOR APPLICATION NUMBER: US 60/080,496
PRIOR APPLICATION NUMBER: US 60/080,606
PRIOR PELING DATE: 1999-04-01
PRIOR PILING DATE: 1999-04-01
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-05-07
NUMBER OF SEC ID NOS: 22
SOFTWARE: PATENTIN VETRION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.0%; Score 405; DB 4; Length 330; 32.8%; Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                            293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                     289 VIGNIQVSDDLDEITWILAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches
                                                                                                                                                                                             US-10-278-946-16
; Sequence 16, Application US/10278946
; Patent No. 6821754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.8
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-107-532A-4516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 16
LENGTH: 330
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ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEGKKRIEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSDD-----VTKGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPV 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 --DDQIEASTHGQS-----VSYEYVLEKNPDILFVVDRTKAIGGDDSKDDISANEL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VRGLKILSVIGLLFVLIATAACG--NNSSSNSSKESS---KDGVEIKHEEG-TTKVPKHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRVVVLEYSFVDALVALDV - - KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEBI
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 18.2%; Score 307.5; DB 4; Local Similarity 31.3%; Pred. No. 2.2e-17; nes 107; Conservative 65; Mismatches 123;
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTOREY/AGENT INFORMATION:
REGISTRATION: PAMELE DENEK
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...352
; SEQUENCE DESCRIPTION: SEQ ID NO: 4516:
US-09-107-532A-4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                            100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4516:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781)893-8277
                                                                                                                 CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 -TISKALGKEREGKKRLEEHDKKIREYKKEIIMDKNOKVLPAVAAKSGLLAH-PSNSYVG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 LIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAF----KTISKALGKEBEGKKRL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                    239 GLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLNAVK 294
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Facetic No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: 08/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NOS: 4472
SEQ ID NO 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYT-----SVGTRKQPNLEEISKLKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LLSLVLVLTACSNSSNNNSTSKKKNSDSKETVTIKNSFBASGKENNGSDKKKISNTVEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 KNPKNAVVLDYGALDVL----KELGVADKVKGLPKGENNOSLPKFLDEFKDDKYINTGN
                                                                                                                 9 KILSVIGLLFVLIATAACGNNSSSNSSKBSSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
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                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 347;
                                Score 296; DB 4; Length 351;
Pred. No. 2e-16;
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28.5%; Pred. No. 4.1e-16;
tive 68; Mismatches 121; Indels
                                                                          66; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 LLFVLIATAACGNNSSSNSSKE----SSKDGVEIKHE-----
                                     17.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                            Query Match
Best Local Similarity 29.24
Marches 90, Conservative
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US-09-543-681A-6862
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Matches 101;
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Best Local
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Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT PELLING DATE: 2000-04-05

PRIOR PRILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6862
                                                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5492
LENGTH: 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 NENI--DAFK---TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLAH-PSNSYVGQPLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP----- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDNLIKDMKKYTENLGKIYDKEDKAKKINKDLDRKISDMKDK-TKDFNKKVMYLLVNEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVAHMKKTVLFLLLSLVLVLTACSNSSNNNSTSKKKNSDSKETVTIKNSFEASGKENNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNK-----KNRIIKPLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVEIKHE----
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
17.5%; Score 296.5; DB 3; Length 3
Best Local Similarity 28.4%; Pred. No. 1.8e-16;
Matches 104; Conservative 70; Mismatches 131; Indels
                                Sequence 5492, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Staphylococcus epidermidis US-09-134-001C-5492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 LVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDELNE 344
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US-09-543-681A-6862
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Rockville
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: 611 H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 LVFDTLGFKPA------DKKVSKSPHGQNINNEYINKQNPDVILAMDRGSVVGGKATT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 RKQPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENI--DAFK-- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 KHPKRVVVLEYSFVDALVALDVKPVGIADDNK-----KNRIIKPLRD--KIGKYTSVGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 -TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAH-PSNSYVG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 QFLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP-----ERMFIMTNKASS 273
                     --ERMFIMTNKASS 273
                                        242 LVFDTLGFKPA-----DKKVSKSPHCQNINNEXINKQNPDVILAMDRGSVVGGKATT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EGTTKVP 55
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                                                                                                                                                                                              Sequence 1268, Application US/09710279

Ratent No. 6703492

GRNERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: 60164,258
PRIOR APPLICATION NUMBER: 60164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 NEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSK 327
                                                                                                         274 NEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Artificial Sequence: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.3%; Score 292; DB 4; Length 347; Best Local Similarity 28.5%; Pred. No. 4.1e-16; Matches 101; Conservative 68; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LLFVLIATAACGNNSSSNSSKE----SSKDGVEIKHE------
                     221 QFLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Arti: OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-710-279-1268
                                                                                                                                                                         RESULT 9
US-09-710-279-1268
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B: Human Genome Sciences, Inc. 9410 Key West Avenue

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Sequence 4342, Application US/09134000C

Patent No. 6617156
GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSOLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|:| : ||:
EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSVIGLLFVLJATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 317;
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                                                                                      3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 283; DB 4; L. 30.4%; Pred. No. 2e-15; tive 59; Mismatches 130;
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                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 amino acids
                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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Best Local Similarity
Maryland
                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
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                     USA
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US-09-071-035-40

Sequence 40, Application US/09071035

Sequence 40, Application US/09071035

Patent No. 64404040

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Bnterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:

ADDRESSES: Human Genome Sciences, Inc.
                                                                                                         288
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                                                   81 GIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GAPTKN-----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLIII-SGRQQDYQEQLKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 IAPTIEL----KSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIBEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 LEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVT 237
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                                                                                                       --KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKE--LEKDPVWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 CGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV--KPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: H9 Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                    287 TTSAYKNGGIVYLOSDLWYLSGGGLESLTQQIEAVQ 322
                                                                                                                                                                                              289 KLNAVKNQRVDILDRDLWARSRGLISSBEMAKELVE 324
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APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,373
REPERBNCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (301) 309-8504
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: A. Anders Brookes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                           KGLSKYL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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APPLICANT: GARY BRETON:
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: US/09/543,681A
CURRENT PELICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                       68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII 125
                                                                                                                                                                                                                                                                                                                                                                                               :|:| : ||: || | | | : : | |: EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VŢ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 HGQS------VSYEYVLEKKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKND 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DFGLYDSLVALGLADKVVGLPLGNAPEYIKGRIANDV-----ANVGGMKAPDFERLAE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 LKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDA-FKTISKALGKEEBGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                               11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEBGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KILSVIGLLFVLIATAACGNNSS----SNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 325;
                                                                                                                                                                                            Length 327;
                                                                                                                                                                                          Query Match 16.7%; Score 283; DB 4; Length 32' Best Local Similarity 30.4%; Pred. No. 2.1e-15; Matches 101; Conservative 59; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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28.0%; Pred. No. 4.9e-15;
:ive 65; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5565, Application US/09543681A Patent No. 6605709
                                                                                                                         ORGANISM: Enterococcus faecalis
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4342
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
US-09-543-681A-5565
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                                                                                                                                                 US-09-134-000C-4342
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Best Local
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 TMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 TETLSQVNPERMFI-----MTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-27
PRIOR PELING DATE: 1999-08-27
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PRIOR PELING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR PELICATION NUMBER: DE 19941378.9
PRIOR PELICATION NUMBER: DE 19941378.9
PRIOR PELICATION NUMBER: DE 19941379.7
PRIOR PELICATION NUMBER: DE 19941379.7
PRIOR PELICATION NUMBER: DE 19942077.7
PRIOR PELING DATE: 1999-09-03
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DE 19940765.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 WVSGVGPLGGSKVLEDI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARSRGLISSEEMAKEL 322
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25.9%;
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Best Local Similarity 25.9*
Matches 82, Conservative
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ORGANISM:
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                                                                                                                                                                         220 YEYVLEKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKNDKVIMLQPDVWYLSGG 279
   NOKVLPAVAAKSGILAHPSNSYVGQFLSQIGFKEALSDD----VTKGLSKYLKGPYLOMN 252
                                                                                                                                253 TETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRG 311
                                                                SA-----
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APPLICANT: Sch"der, Hartwig
APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Conversion Conversion General Conversion Fire Of Invention: Involved In Membrane Synthesis and Membrane
TITLE OF INVENTION: TRANSPORT
FILE REPERENCE: BG1-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
                                                                172 N-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEASTHGQS
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PRIOR FILING DATE: 1999-06-25

PRIOR PELING DATE: 1999-07-08

PRIOR PELING DATE: 1999-07-09

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FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 572, Application US/09602787A Patent No. 6696561
                                                                                                                                                                                                                                                                 312 LISSEEMAKELVELSKK 328
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280 GLESMHL---MIEDVKK 293
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APPLICANT: Pompejus, Mark
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Sequence 2977, Application US/09583110

Sequence 2977, Application US/09583110

Sequence 2977, Application US/09583110

Sequence 2977, Application US/09583110

Sequence 2977, Application

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: NUMBER: US/09/583,110

CURRENT FALING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

SEQ ID NOS: 5322
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Patent No. 6800744

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

THEORY OF THE OF THEORY TO STREPTOCOCCUS PREUMONIAE

THEORY OF THE OF THEORY TO STREPTOCOCCUS PREUMONIAE

THEORY OF THE OF THEORY TO STREPTOCOCCUS PREUMONIAE

THEORY OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 LLLLGACSTNSSTSQTETSSSAPTEVTIKSSLDEVKLSKVPEKIVTFDLGAADTIRALGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 321
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 NAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.8%; Score 250; DB 4; 27.2%; Pred. No. 1.1e-12;
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STATE: Massachusetts
COUNTRY: USA
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MEDIUM TYPE: CD/ROM
COMPUTER: <Unknown>
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Best Local Similarity 27.2*
Matches 92; Conservative
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US-09-107-433-4809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3723, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ELIKNTEARISKELEKH----PEIKGKI----KGKKVLPTMINAADTSKFWIYTSKDPRAN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DALVALDVKPVGIADDN----KKNRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVALALGIVPVGFSKANYGVSADKGVLPWTEEKIKELNGKANLFDDLDGLNFEAISNSKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLIIADNNRHKGI----YKDLNKIAPTIELKSFDGDYNENI--DAFKTISKALGKEEEG- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLSQLG--FKEALSDDVTKGLSKYLKGPYLQMNTFTLSQVNPERMFIMTNKASSNEPSLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KKRLEEHDKKIEEYKKEITMDKNQKVLPAV---AAKSGLLAHPSNSYVGQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LIAILAMCIVPSACSSNSVKNEENTSKEHAPDKIVLDHAFGQTILDKKPERVATIAMGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VIGLLFVLIATAACGNNS---SSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 ELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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28.9%; Pred. No. 5.5e-13;
tive 58; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                       15.7%; Score 265; DB 3;
llarity 92.9%; Pred. No. 6.3e-15;
Conservative 2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 ELEKDPVWKKLNAVKNORVDIL 301
                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        j ORGANISM: Streptococcus pneumoniae
US-09-583-110-3723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Conservative
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Best Local
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CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR PILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PAPLICATION NUMBER: DE 19931478.0
PRIOR PAPLICATION NUMBER: DE 19931553.9
PRIOR PAPLICATION NUMBER: DE 1993122.1
PRIOR PILING DATE: 1999-07-09
PRIOR PELING DATE: 1999-07-09
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR FILING DATE: 1999-07-09

R FILING DATE: 1999-07-09

R APPLICATION NUMBER: DE 19932191.4

R FILING DATE: 1999-07-09

R FILING DATE: 1999-07-09

R APPLICATION NUMBER: DE 19932209.0

R APPLICATION NUMBER: DE 19932212.0

R RILING DATE: 1999-07-09

R RPLING DATE: 1999-07-09

R PILING DATE: 1999-07-09

R PILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19942079.3
FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: DE 19932228.7
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932229.5
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 1993230.9
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: DE 19940766.5
FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940830.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940831.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940832.7
FILING DATE: 1999-08-27
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APPLICATION NUMBER: DE 19941378.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19940833.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: DE 19941395.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE 19942078.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: DE 19932927.3
FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE 19933005.0
FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940765.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DE 19933006.9
FILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: DE 19940764.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 KPVGIADDNKKNRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 HKGIYKDLNKIAPTIELKSFDGDYNENIDA-PKTISKALGK--EEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 Y-----KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSO-LGFKEALSDDVTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 GLSKYLKGPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWKKL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 VATKNESSDKKALAILLNEGKMAAFGAKSRF-----SFLYOTLKFKPT---DTTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LLLLGACSTNSSTSQTETSSSAPTEVTIKSSLDEVKLSKVPEKIVTFDLGAADTIRALGF
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APPLICANT: Kr"ger, Burkhard
APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: CORYNEACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapg
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14.8%; Score 250; DB 4; Length 325;
Best Local Similarity 27.2%; Pred. No. 1.1e-12;
Matches 92; Conservative 65; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 NAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
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                            SOFTWARE: cUnknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...325
SEQUENCE DESCRIPTION: SEQ ID NO: 4809:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 598, Application US/09602787A Patent No. 6696561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 325 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781) 893-8277 INFORMATION FOR SEQ ID NO: 4809: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-602-787A-598
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Sequence 70, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                      295
242
                                                                                                           243 -----QPISSEFIKKADPDILYIVDRTAVMEHRSNINAASV----ENPLLRQTKAWKN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 RVVVILEYSFV-DALVALDVKPVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKQPNL-- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LKILSVIG--LLFVLIATAACGN-NSSSNSSKESSKDGVEIKHEEGTT-----KVPKHPK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LKKTVLIGTTLLLGSFLLAACGNTNKEANNADKT------HEVTDTLGNKVTVPAKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ----EBISKLKPDLIIADNNR--HKGIYKDLNKIAPTIELKSFDGDYNENI----DAFKTI
186 QVKQV-QAVTANRPERALVVLHNNGAFSNFGIQSRYGFIFNAFGVKPASGVVDTSLHG--
                                                                  242 KYLKGPYLQMNTETLSQVNPERMFI-----MTNKASSNEPSLKELEKDPVWKKLNAVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKALGKEBEGKKRLEEHD---KKIBEY--KKEITMDKNQKVLPAVAAKSGLLAHPSNSYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
                                                                                                                                                                                                                                                     296 QRVDILDRDLWARSRGLISSEEMAKELVE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PB.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 70:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.3%;
Matches 98; Conservative 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT 21
US-09-071-035-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-071-035-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTO9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 VLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKI--GK-YTSVGTRKQPNLEEISKL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 TLGVIDADIVLALGTVPVGNTGYKFFENGLGPWTDELVEGKELTLLDSDSTPDLEQVAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||||| : ::|:|| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 LEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHP----SNSYV----GQFLSQLGF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDP 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 KGIYKDLNKIAPTIELKSFDGDYNEN------IDAFKTISKALGKEEEGKKRLEEHDK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIERYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEA--LSDDVTKGLS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KPDLIIADNNRHKG-IYKDLNKIAPTIELKSFDGDYN-ENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KILRSSVVGVA-VLALLAGCSNNADDIDADSTSTGNSAFPVSIEHEFGTTTIDDVPERVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 NEETDALIQAAR----DEN----PSFDGKTGTVILPYQGKYGAYLPGDARGQFLDSLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 SLPEAVLSRDTGDSF-----FVDVPAESVKDVDGDVLVL----SNDENLDITAENP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KIL--SVIGLLFVLIATAACGNNS----SSNSSKESSKDGVEIKHEEGTTKVPKHPKRVV
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 VWKKINAVKNORVDILDRDLWARSRGLI-----SSEEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                             29;
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14.3%; Score 241; DB 4; Length 324;
1 Similarity 24.0%; Pred. No. 6e-12;
79; Conservative 77; Mismatches 135; Indels 38;
                                                                                                                                                                                                                                                                                          Length 332;
                                                                                                                                                                                                                                                                               ch 14.6%; Score 246.5; DB 4; Length 3 il Similarity 26.7%; Pred. No. 2.2e-12; 94; Conservative 70; Mismatches 129; Indels
                                                                                                                                             1 TYPE: PRT
7 ORGANISM: Corynebacterium glutamicum
U8-09-602-787A-598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Acinetobacter baumannii
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 678
SEQ ID NO 598
LENGTH: 332
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Best Local Similarity
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US-09-328-352-4444
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                                                                                                                                                                                                                                                                                          Query Match
Best Local (
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189 KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSO-LGFK--EALSDDVTKGLSKYLK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 KKNRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLN 139
246 GPYLOMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWKKLLNAVKNOR 297
                                        ---AAKNGK 267
                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 NSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 KIAPTIELKSFDGDYNENIDA-FKTISKALGK--EEEGKKRLEEHDKKIEEY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOSTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIPICATION: CUNROWN>
PRIOR APPLICATION: CUNROWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.0%; Score 236; DB 4; Length 298;
Best Local Similarity 26.6%; Pred. No. 1.4e-11;
Matches 88; Conservative 65; Mismatches 112; Indels
                         ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                298 VDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                         268 IIQLTPDLWYLSGGGLESTKLMIEDIQKALK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                       ; Sequence 24, Application US/09536784; Patent No. 6573082; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 298 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                     RESULT 23
US-09-536-784-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-536-784-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQ-LGFK--EALSDDVTKGLSKYLK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                           -----GOFLSQ-LGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                         270 KASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                  KKONRIIKP-----LRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 BIAPTVLFQASKDDYWTSTKANIESLASAFGETGTQKAKEELTKLDKSIQEVATKNESSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 NSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGLADDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKALAILLNEGKMAAFGAKSRF-----SFLYQTLKFKPTDTKFEDSRHG----
                                                  203 FMVSDNRSSGTVLYQDLGLQ---VPKLVEEISKNATADMNQVSLEKLAELDADHIFLVNS
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAPTIELKSFDGDYNENIDA-FKTISKALGK--EEEGKKRLEEHDKKIEEY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 3;
1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 236; 26.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/961,083
                                                                                                                                                                                                                                                    Sequence 24, Application US/08961083 Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION UNDRER: 36,373
REFERENCE, DOCKET UNDRER: PB34,
TELECOMMUNICATION INFORMATION:
TELEPHOR: (301): 309-8504
TELEFAX: (301): 309-8512
INPORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-961-083-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 88; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20850
                                                                                                                                                                                                              RESULT 22
US-08-961-083-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
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Gaps

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US-09-302-626B-12
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US-09-071-035-72
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Sequence 72, Application US/09071035

Sequence 72, Application US/09071035

Setent No. 6448043

GENERAL INFORMATION:
APPLICANT: G11 H. Choi
TITLE OF INVENTION: Enterococcus faccalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCES: 496
CORRESPONDENCES: 496
CORRESPONDENCES: 9410 Key West Avenue
CITY: ROCKVILLE
STREET: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BNIEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT PILING DATE: 1998-08-13
FRICR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 VKPVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKQPNL-----EEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 NNR--HKGIYKDLNKIAPTIELKSFDGDYNENI---DAFKTISKALGKEEGKKRLEEHD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 ---KKIEEY--KKEITMDKNQKVLPAVAAKSGLLAHPSNSYV------GOFLSQ-LG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 TLTKGVQEYLGKKD-----AGKSAAVLWVTNNQVFMVSDNRSSGTVLYQDLG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 FKEALSDDVTKGLSKYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW 287
246 GPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWKKLNAVKNQR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AACGNINKEANNADKI------HEVIDILGNKVIVPAKPKRIIA---SYLEDYLVALG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AACGN-NSSNSSKESSKDGVEIKHEEGTT----KVPKHPKRVVVLEYSFV-DALVALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 236; DB 4; Length 301; 27.0%; Pred. No. 1.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNLPAVKNNQVHTYDK----KSSWLYNGPIANTQIVEDVKK 297
                                                                                              268 IIQLTPDLWYLSGGGLESTKLMIEDIQKALK 298
                                                                        298 VDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Mismatches
                                                                                                                                                                                                  Sequence 6014, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Conservative
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US-09-071-035-72
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Matches 9
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79 PVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKOPNL-----EEISKLKPDLIIADNN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 BALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 R--HKGIYKDLNKIAPTIELKSFDGDYNENI---DAFKTISKALGKBEBGKKRLBEHD-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 CGN-NSSSNSSKESSKDGVEIKHEEGTT----KVPKHPKRVVVLEYSFV-DALVALDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 -KKIEEY--KKEITMDKNQKVLPAVAAKSGLLAHPSNSYV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAVKNNQVHTYDK----KSSWLYNGPIANTQIVEDVKK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 LNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.5%; Score 228; DB 4; 26.5%; Pred. No. 6.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Scalato, Enzo
APPLICANT: Masignani, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITE OP INVENTION: Meningococcal Antigens
FILE REPERENCE: CHIROLS9
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/POCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 12, Application US/09302626B
; Patent No. 6709660
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 amino acids
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Best Local Similarity 26.5%
Matches 90, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                         FILING DATE:
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19,

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184 A-AKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGV-PAVDESIKEGSHGQ--- 238
                                                                                                                                                                                                                                                                                                                                                                                                                                :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : : | : | : : | : | : : | : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : : | : : : | : : : : | : : : : | : : :
                                                                                          247 PYLOMNTETLSQVNPERMFIMTNKASSNE--PSLKELEKDPVWKKLNAVKNQRVDILDRD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                    -IDAFKTISKALGKEEEGKKRLEEHDKKIE
                                                                                                                                                                                                                187 EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5206
CORRESPONDENCE BADDRESSE:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: MAy 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...295
SEQUENCE DESCRIPTION: SEQ ID NO: 4519:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 TYLAAGG-----AQELLNASKQ 312
                                             HKGI YKDLNKI APTI ELKSFDGDYNEN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 LWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: CD/ROM ISO9660
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OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4519, Application US/09107433; Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 295 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (781)893-8277
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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COMPUTER READABLE FORM
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Best Local Similarity 28.09
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 HKGIYKDLNKIAPTIELKSFDGDYNEN----IDAPKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AKAPDK-LNEIAPTIEMTADTANLKESAKERIDA---LAQIFGKKAEADKLKAEIDASFE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 A-AKTAAQGKGKGLVILVNGGKMSAFGPSSRLGGWLHKDIGVPAV--DEAIK-----EG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 PYLQ-MNTETLSQVNPERMFIMTNKASSNE--PSLKELEKDPVWKKLNAVKNQRVDILDR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 SHGQPISFEYLKEKAMPDWLFVLDRSAAIGEEGQAAKDVLNNPLVAETTAWKKGQVVYLVP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | | : | | : | | : : | | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : : | | : : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Bizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REPERENCE: CHIROLS9
CURRENT APPLICATION NUMBER: US/09/302,626B
CURRENT PILING DATE: 1999-04-30
PRIOR PELING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.9%; Score 218; DB
Best Local Similarity 27.1%; Pred. No. 4.7e
Matches 88; Conservative 63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 ETYLAAGG-----AQELLNASKQ 312
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APPLICANT: Scalato, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis
                                                                                                                                                                                                                                                                  ORGANISM: Neisseria meningitidis
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 321
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Matches 85; Conservative
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Sequence 5819, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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ORGANISM: Staphylococcus epidermidis
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STATE: Massachusetts
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                   |||| |:::| |
264 AVKNTRIETVDGD 276
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292 AVKNORVDILDRD 304
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                                                                                   RESULT 30
US-09-134-001C-5667
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                                                                                                                                                                                                                                              184 ELIKNTEARISKELEKH----PEIKGKI----KGKKVLFTMINAADTSKFWIYTSKDPRAN 236
                                                                                                                                                                                                                                                                                                                   69 VDALVAL----DVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQ-----PNLEEISKL 119
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                                                                                                                                                       DLIIADNNRHKGI----YKDLNKIAPTIELKSFDGDYNENI--DAFKTISKALGKEEEG- 174
                                                                                                                                                                                        130 DVILAG---YSGITKEDYDTLSKIAPVAAYKSKPW---QTLWRDMIKIDSKALGMEKEGD 183
                                                                                                                                                                                                                                                                                             FLSQLG--FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLK 279
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                                     APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INYENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INYENTION OF STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILLING DATE: 2000-11-09
PRIOR PILLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PREGETIN Ver. 2.1
SEQ ID NO 1888
LENGTH: 299
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                                                                                   DALVALDVKPVGIADDN---KKNRIIKP-
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Patent No. 6703492
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US-09-710-279-1888
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Matches 79
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Sequence 5667, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.2%; Score 205.5; DB 3; Best Local Similarity 25.2%; Pred. No. 4.8e-09; Matches 79; Conservative 62; Mismatches 111;
```

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44 EIKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 S----VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DA-FKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : || ||: | :: || |: | :: || |: | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 ELKHETGTLSVPATPSRLAVYDLGVLDTLNALGIRAVAVPK-----ATFPATLSAXN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IATAACG--NNSSSNSSKE----SSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDA
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10.7%; Score 181.5; DB 4; Length 240;
Best Local Similarity 32.2%; Pred. No. 3.2e-07;
Matches 59; Conservative 34; Mismatches 67; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: ORF38a US-09-302-626B-159
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 185; DB 4; Length 316;
; Pred. No. 2.4e-07;
51; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 NKASS---NEPSLKELEKDPVWKKLNAVKNORVDILDRDLW 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:: | | | :: | | | 253 RGAATGGGENKALETLAKHPELSQTRAFKQGRVIVVDAPSW 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 159, Application US/09302626B
; Sequence 159, Application US/09302626B
; Retent No. 6709660
; GENERAL INFORMATION:
    APPLICANT: Scalato, Enzo
; APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Rappuoli, Rino
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FILE REFRENCE: CHIROLS9
; CURRENT APPLICATION NUMBER: US/09/302,626B
; CURRENT FILING DATE: 1999-04-30
; PRIOR PILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
FRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.8%;
Matches 64; Conservative 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Myxococcus xanthus US-09-902-540-9745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-302-626B-159
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LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 G---IADDNKKARIIKPLRDKIGKYTSVGTRKQPNL-----EEISKLKPDLIIADNNR- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 -HKGIYKDLNKIAPTIELKS-PDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----WKNLKA 303
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Batent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 TAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVV--VLEYSFVDALVALDVKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 AQWTVGSGSIQDYLQDDLKD------VPTISYDLPYEKVLSFEPDLLLISSSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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11.5%; Score 194.5; DB 4; Length 338;
Best Local Similarity 23.4%; Pred. No. 4.4e-08;
Matches 78; Conservative 69; Mismatches 107; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------WSAVSSEKLAELDADYIILVNSDKDAAMFNEPS
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                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atiniallo, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-012
                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...338
;
SEQUENCE DESCRIPTION: SEQ ID NO: 5819:
US-09-107-532A-5819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (701)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 5819:
SEQUENCE CHARACTERISTICS:
ELENGTH: 338 amino acids
TYPE: amino acids
                      MEDIUM TYPE: CD/ROM ISO9660
                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 32
US-09-902-540-9745
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GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 LSKLGVK-TGLSVD--KNRL--PYLEEYFKTTKPAGTLFEPDYETLNAYKPQLIIIGSRA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 NPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLPAVAAKSGLLAHPSNSYVGQFLSQLGFKBALSDDVTKGLSKYLKGPYLQMNTETLSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IATAACG--NNSSSNSSKESSKD-----GVEIKHEEGTTKVPKHPKRVVVLEYSFVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LALGACSPONSDSAPQAKEQAVSAAQTEGASVTVKTARGDVQIPQNPERIAVYDLGMLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 VPKHPKRVVVLEYSFVDALVALDVKP--VGIADDNKKNRIIKP----LRDKIGKYTSVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 HKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.1%; Score 153; DB 4;
Best Local Similarity 30.1%; Pred. No. 4.3e-05;
Matches 47; Conservative 31; Mismatches 62
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: PCT/IB99/00103
PRIOR FILING DATE: 1999-01-14
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7331, Application US/09489039A Patent No. 6610836
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                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (142)..(143)
CTHER INFORMATION: unknown
US-09-302-6268-8
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Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
US-09-489-039A-7331
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US-09-489-039A-7331
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                                                                                                                                                                                                                         LENGTH: 164
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                                                                                                                                                                                                                                                                 TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILLE DEPLICATION NUMBER: US 60/117,747
PRIOR PLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 LVALDVKPVGIADDNKKNRIIKPLRDKIG---KYTSVG-TRK------QPNLEBISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSDDVTKGLSKYLKGPYLQMNTETLSQ-VNPERMFIMTNKASSNEPSLKELEKDPVWKKL 290
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           73 LSKLGVK-TGLSVD--KNRL--PYLEBYFKTTKPAGTLFEPDYETLNAYKPQLIIIGSRA 127
                                                                                 HKGIYKDLNKIAPTIELKSFDGDYNEN----IDAFKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                                                               128 AKAFDK-LNEIAPTIEMTADTANLKESAKERIDA---LAQIFGKKAEADKLKAEIDASFE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDLILVSATGGDSALPLYDQLKTIAPTLVINYDDKSWQTLLTQLGQIT---GHEQQASAR 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDLIIAD --- NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 157.5; DB 4 22.1%; Pred. No. 4.9e-05;
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APPLICANT: Scalato, Enzo
APPLICANT: Radignali, Vega
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
APPLICANT: Grandi, Guido
TITLE OF INVENTION: Meningococcal Antigens
FIRE REPERENCE: CHIROLS9
CURRENT APPLICATION NUMBER: US/09/302,626B
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6610836
GENERAL INFORMATION:
APPLITANT
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Patent No. 6709660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13095
LENGTH: 337
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Matches 68, Conserv
                                                                                                                                                                                                                             187 EYK 189
                                                                                                                                                                                                                                                                                                   184 AAK 186
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US-09-489-039A-13095
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US-09-302-626B-8
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7262
LENGTH: 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 KLKPDLIIADNNRHKGIYKDLNKIAPTIE-LKSF------DGDYNENIDAFKTISKAL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 QLGFKEALSDDVTKGLSKYLKGPY-----LOMVTETLSQVNPERMFIMTNKASSNE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 TSG-RESITNDFIE-----LAGAYNIVQTNANQPNVNPETLIEWNPDNIVLW-----NTN 275
                                                                                                                                                                                                                                              89 NRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELK 148
                                                                                                                                                                                                                                                                                                                                                        207 KSG-LLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGPYLQMNTETLSQVN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GORIDVSAEQLPELD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDALVALDV--KPVGIADD-----NKKNRIIKPLRDKIGKYTSVGTRKQPNLEBIS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 LLKPDLVIVGSGQ-----TQTIELLROFGIAVYVMESGTYKQVKEELSEIAILS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYV----GQFLS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 IMKLLASLLTLLLLCGCSSSEQNRKTQENSTSHSICVFDSTNTKVCVAKPAQRIVSLFES
                                                                                                                                                                                                     84 TVTVPLHPQRIVSMHDLDITIPLIELGAPPIASHGRTRPDGSHYLRSSAQLTGVDFDNSD
                                                                                                                                                                                                                                                                      10 ILSVIGILFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTK--VPKHPKRVVVLEYS
                                                                                                                                                                --GIADDNKK
                                                                                                                                                                                                                                                                                                                                149 SPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKN--QKVLPAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                       63;
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                                                                             Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 140.5; DB 4; Length 3:
; Pred. No. 0.0013;
56; Mismatches 113; Indels
                                                                                                                       Indels
                                                                         ; Score 143.5; DB 4;
; Pred. No. 0.00079;
47; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 NNGKVTVHHSYHALGRVLRDAGFRFPPLIERIPD----
                                                                                                                                                           51 TTKVPKHPKRVVVL-EYSFVDALVALDVKPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSL----KELEKDPVWKKLNAVKNQRV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7262, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Acinetobacter baumannii US-09-328-352-7262
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 ADFVFATWRSDTGGKP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 PERMFIMTNKASSNEP 276
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Best Local Similarity 22...
Best Tocal Similarity 22...
Then 75; Conservative
                                                                             Query Match
Best Local Similarity 21.9*
Matches 56; Conservative
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US-09-328-352-7262
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                                                                                                                                                                                     Sequence 12270, Application US/09489039A
Sequence 12270, Application US/09489039A
Patent No. 6610836
EGENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6610836
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILIS OF ACID.
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
FRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7324
LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 YVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 LFQEVLDRFGIKNAWHGEAAFWGS------VSVGIDRLAAFNEADVICFDH---GNERD 302
  303 NPQVIFVQDRYPQ----VVKQIENDPQWQAIDAVKHHVWLMPE--YAKAWGYPMPEALA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------PKRVVVLEYSFVDALVALDVKPVGIAD-DNKKNRIIKP-LRDKIG 100
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8.5%; Score 144; DB 4; Length 353;
Best Local Similarity 20.9%; Pred. No. 0.00067;
Matches 67; Conservative 52; Mismatches 137; Indels
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                                                                   320 KELVELSKK 328
                                                                                                       357 LGELWMAKK 365
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US-09-489-039A-7324
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67 74

Gaps

276 PKLIYERKELQ-----GLSAVQNRKV 296

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| Sequence 194, Application US/08961083 |
| Sequence 194, Application US/08961083 |
| Sequence 194, Application US/08961083 |
| Patent No. 615946 |
| GARBAAL INCORMATION: Streptococcus pneumoniae Antigens and Vaccines ADPLICANT: Choi et. al. |
| ITHE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines CORRESPONDENCE ADDRESSE: |
| ADDRESSEE: Human Genome Sciences, Inc. |
| STREET: 9410 Key West Avenue |
| STREET: 9410 Key West Avenue |
| STREET: 9410 Key West Avenue |
| COMPUTRY: USA |
| ITHE OF INTERTION OF A COMPUTER READALE FORM: |
| MEDIUM TYPE: Diskette, 3.50 inch, 1.4MD storage |
| COMPUTRY: USA |
| COMPUTRY: USA |
| STATE: MAYOR SYSTEM: MSDOS version 6.2 |
| COMPUTRY: HE VOCITA 486/33 |
| OPERATING SYSTEM: MSDOS version 6.2 |
| OPERATION DATE: |
| SPILING DATE: |
| FILING DATE: |
| FILING DATE: |
| APPLICATION NUMBER: |
| PRICE TOWN DATA: |
| APPLICATION NUMBER: |
| PRICE TOWN NUMBER: |
| PRESERVE FOCKET NUMBER: |
| PRESERVE FOCKET NUMBER: |
| TELECOMMUTATION INFORMATION: |
| TELECOMMUTATION FOR SEQ ID NO: 194: |
| SEQUENCE CHARACTERISTICS: |
| LENGTH 1 312 mino acide |
| TYPE: mino acide |
| TYPE: mino acide |
| TOPOLOGY: | Incary
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7.9%; Score 134; DB 3; Length 132;
Best Local Similarity 30.5%; Pred. No. 0.0012;
Matches 39; Conservative 23; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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120 -YSGITKE 126
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2005, 09:17:46; Search time 65 Seconds (without alignments) 2639.177 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

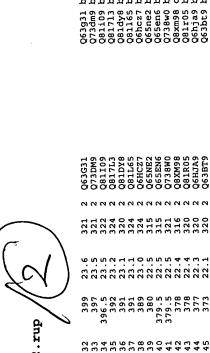
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	crip	1							Q6gah5 staphylococ			Q6gi45 staphylococ							photor	erwinia c							7		_		bacillus .	Q6hnj9 bacillus th
SUMMAKIES	ΩI	QBCNG3	683660	Q7A499	Q6GEQ2	QBNVD6	Q6G7D7	QBNXA6	QGGAHS	Q99V55	Q7A6B6	Q6G145	034348	007616	Q65LP5	Q9CPB7	Q8GRB3	Q87FM4	Q7M254	Q6D898	Q93F19	FECB ECOLI	Q889 <u>T</u> 6	Q65F62	087491	Q7A1Z7	Q7A2Y7	Q7A869	Q6GD10	Q6GKJ0	Q81V85	QCHINJ9
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	* Query Match Length	334	327	327	327	327	327	319	319	319	319	319	315	348	325	298	307	307	302	304			306	325	330	330	330	330	330	330	321	321
	% Query Match	99.5	72.9	72.9	72.8	72.6	72.6	42.9				42.6	40.2	36.2	36.0	30.6	28.9		28.2	28.2	27.4	27.2	26.9	24.6	24.0	24.0	24.0	24.0	24.0	24.0	23.9	23.9
	Score	1681	1232	1232	1230	1227	1227	725.5	725.5	724.5	724.5	719.5	679.5	611	608.5	516.5	488.5	487.5	476	476	463	460	454.5		405	405	405	405	405	405	404.5	404
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## ALIGNMENTS

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3 PRELIMINARY; PRT; 334 AA.	(TrEMBLrel. 23, Creat	01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	er.	OrderedLocusNames=stlos; gtanhvlococcis poidermidis	Bacteria; Firmicutes; Bacillales; Staphylococcus.	NCBI_TaxID=1282;	NCE FROM N.A.	STRAIN=ATCC 12228;	.0922; , Ren SX., Li HL., Wang YX., Fu G., Yang J.,	رق. ر يورون	of virulence genes in a	epidermidis strain (ATCC 12228).	Mol. Microbiol. 49:1577-1593(2003).	F: iron	GO:0006827; P:high affinity iron ion transport; IEA.	InterPro; IPR002491; Peripla BP. Pfam; PF01497; Peripla BP 2; 1.	138 MW	tch 99.5%; Score 1681; DB 2; Length 334;	33; Conservative	2 VESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEGTTKVPKHPKRV	GTTKVPKHPKRV	62 VVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLBEISKLKP	61 VVLEYSFVDALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLBEISKLKP	122 DLIIADNNRHKGIYKOLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH	121 DLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH	182 DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHFSNSYVGOFLSOLGFKEALSDDVTKGLS	181 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLS	242 KYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDIL	241 KYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDIL
LT 1 G3 Q8CNG3	01-MA	01-MA	Ferri	Oraer	Bacte	NCBI [1]	SEQUENCE	STRAI	Zhang	Oin Z	"Geno	Staph	Mol.	GO: GO	8	Inter Pfam;	Complete SEQUENCE	Query Match	Matches										
RESULT QBCNG3 ID Q	45	텀텀	B 8	Z 0	38	X X	RP	2 i	<b>\$</b> \$	A a	<b>\$ 5</b>	RT	38	ž	DR	ᅜ	S KW	88	Ϋ́	ò	q	8	q	ò	qq	ò	Q	ò	qq

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NCBI_TaxID=158879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETALIN=MUSO / ATCC 700639;
MEDILINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Kanahisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Harashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
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EMBL, AP003364; BAB58339.1; -.

PIR; D90013; D90013.

GO; GO:0005381; F: iron ion transporter activity; IEA.

GO; GO:00063827; P: high affinity iron ion transport; IEA.

InterPro; IPR002491; Peripla BP.

Pfam; PF01497; Peripla BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                         327 AA; 36591 MW; 6AEEECBC4E17CDB7 CRC64;
                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to ferrichrome ABC transporter.
                                                                                                                                                           Staphylococcus aureus (strain Muso / ATCC 700699).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
DRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
            DRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 334
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                                                                               327 AA
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                                                                                                                                                  OrderedLocusNames=SAV2177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 71.9
Matches 235, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                              PRELIMINARY;
                                                                                                                                                                                   NCBI_TaxID=158878;
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01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Acki K.-I., Magai Y., Lian J.-Q., Ito T., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanto C., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T., "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 BYSFADALAALDVKPVGIADDGKKKRIIKPVREKIGDYTSVGTRKQPNLEBISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transport system binding lipoprotein.
OrderedLocusNames=SAR2268;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match / 72.9%; Score 1232; DB 2; Best Local Similarity 71.9%; Pred. No. 1.5e-59; Matches 235; Conservative 42; Mismatches 50;
                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus
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PubMed=15213324; DOI=10.1073/pnas.0402521101;
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                                                                                                                                                                                                                     OrderedLocusNames=SA1979;
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Gaps

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64 9 124

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Rangeausinssa; Veries Control of Arkin R., Barron A., Benight M.T.G., Fell E.J., Lindaday J.A., Peacock S.J., Day N.P.J., Baright M.C., Fell E.J., Lindaday J.A., Peacock S.J., Day N.P.J., Barright M.C., Fell E.J., Moore C.E., Hurst L., Atkin R., Barron A., Chillingworth T., Chillingworth T., A churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., A chares K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., A ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.; Stevens K., Whitehead S., Barrell B.G., Ry Spratt B.G., Parkhill J.; Stevens K., Whitehead S., Barrell B.G., Evoc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

ENBL, BX571857, CAG43866.1; -
CGO, GO.0006837; Priron lon transporter activity; IEA.

GO, GO.0006837; Priron lon transporter activity; IEA.

InterPro; IPR002491; Peripla BP.; 1.

Fram, PP04197; Peripla BP.; 1.

Fram, PP04197; Peripla BP.; 1.
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                                                                                                                                               72.6%; Score 1227; DB 2; Length 327; 71.6%; Pred. No. 2.8e-59; ive 42; Mismatches 51; Indels (
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GO; GO:0006827; P:high affinity iron ion transport; IEA. InterPro; IPR002491; Peripla_BP. Pfam; PF01497; Peripla_BP_2; 1. Complete proteome. SEQUENCE 327 AA; 36577 MW; GAEDCDBC4E169CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36577 MW; 6AEDCDBC4E169CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putative transport system binding lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
PubMed=15213324; DOI=10.1073/pnas.0402521101;
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                                                                                                                                                                             71.6%;
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Best Local Similarity 71.6
Matches 234; Conservative
                                                                                                                                                                                                      Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 304
                           Enright M.C., Foster T.J., Minusay U.M., Feature, S.J., Akkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quall M.A., Rabbinowitsch B., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitchead S., Barrell B.G., Spart B.G., Parkhill J.; Rabbinowitsch B., Rutherford K.M., Sanders M., Spratt B.G., Parkhill J.; Nhitchead S., Barrell B.G., Spratt B.G., Darkhill J.; Longlete genomes of two clinical Staphylococcus aureus strains:

"Complete genomes of two clinical Staphylococcus aureus strains:
proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).

ROJ. GO:0005381; Filon of transporter activity; IEA.

GO; GO:0005827; Phigh affainty iron ion transport; IEA.

Roy, GO:0006827; Phigh affainty iron ion transport; IEA.

Roy, GO:0006827; Phigh affainty iron ion transport; IEA.

Roy, GO:0006827; Phigh affainty iron ion transport; RAM.

Roy, GO:0006827; Phigh affainty iron ion transport; RAM.

Romplete proteome.

Romplete proteome.
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MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
MEDLINE=22040717; PubMed F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EYSFADALAALDVKPVGIADDGKKKRIIKPVREKIRDYTSVGTRKQPNLEEISKLKPDLI
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               Peacock S.J., Day N.P.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.8%; Score 1230; DB 2; Length 3 Best Local Similarity 72.2%; Pred. No. 1.9e-59; Matches 236; Conservative 39; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome and virulence determinants of high virulence acquired MRSA.";
Lancet 359:1819-1827(2002).
EMBL, AP004829; BAB95966.1; -.
GO, GO:0005381; F:iron ion transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=196620;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
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OrderedLocusNames=MW2103;
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PubMed=1521324; DOI-10.1073/pnas.0402521101;

Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

A Baright M. C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

Bason N., Bentley S.D., Chillingworth T.,

Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A chares K.D., Lennard M., Line A., Mayes R., Moule S., Mangall K.,

Ormond D., Quall M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,

Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.;

"Complete genomes of two clinical Staphylococcus aureus strains:

"The Fool Natl. Acad. Sci. U. S.A. 101:9786-9791(2004).

B. MBL; BX571857; CAG42748.1; -

GO; GO:0005821; Fifon ion transporter activity; IEA.

RO; GO:0005827; Pihigh affinity iron ion transport; IEA.

Prim; PRO1997; Peripla BP. 2:

ROMPLEE PRO1497; Peripla BP. 2:

ROMPLEE PRO149
EQSTLKSAFAFGISRAGMFINNEDTFWGQFLLKMGIQPEVTKDKTTHVGERKGGPYIYLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain MSSA476).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282459;
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Pred. No. 5.7e-32;
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QGGAHS;
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                                                                          VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK
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MEDLINE-22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Takeuchi F., Kasano K., Naimi T., Kuroda H., Cui L.,
Yamamoro K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
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                                           VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
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Lancet 359:1819-1827(2002).
Lancet 359:1819-1827(2002).
EMBL, AP004625; BAB94786.1; -.
GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
Interpro; IPR002491; Peripla_BP.
Pfam; PP01497; Peripla_BP_2; 1.
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
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73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR 310
                                                                                                                                                                MEDLINE=21111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Magai Y., Lian J.-Q., Ito T., Kanamori M., Mateumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Rantori M., Ogasawara N., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Hungashi B., Goto S., Sabuzaki J., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15213324; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil B.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 319;
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EMBL, AP003132; BAB42136.1; -...

EO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006827; P:high affinity iron ion transport; IEA.

InterPro; IPR002491; Peripla_BP.

Pfam; PP01497; Peripla_BP_2; 1.

Complete proteome.

SEQUENCE 319 AA; 35566 MW; DE6D7C7AB4831574 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transport system extracellular binding lipoprotein.
      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus (strain MRSA252).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=282458;
                                                             Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=155879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.9%; Score 724.5; DB 246.9%; Pred. No. 6.5e-32;
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GIIASESMAEDLEKIAEK 317
05-JUL-2004 (TrEMBLrel. 27,
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                                SA0891 protein.
OrderedLocusNames=SA0891;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR 310
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SERAIN=MUSO / ATCC 700699;

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-C., Itc T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 VVFMLILVVAVAVGGGKDT-----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 EQSTLKSAFAFGISRAGMFINNEDTFMGÖFLIKMGIQPEVTKDKTTHVGERKGGPYIYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iron ion transport; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 AA; 35566 MW; DE6D7C7AB4831574 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet 357:1225-1240(2001).

EMBL, AP003361; BAB57200.1; -.

PIR; B89872; E89872.

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:006827; P:high affinity iron ion transport; I
InterPro; IPR002491; Peripla_BP.

Pfam; PF01497; Peripla_BP_2; 1.
                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                          Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.9%; Score 724.5; DB 2;
46.9%; Pred. No. 6.5e-32;
iive 63; Mismatches 95;
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Last sequence update)
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                                                                                                                                                              Created)
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                                                                                                                                                                                                                                               OrderedLocusNames=SAV1038;
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Best Local Similarity 46.9
Matches 149; Conservative
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                                                                                                                                                                                                                                                                        64 AALDMKPVGIADDGSTKNITKSVRDKIGAYESVGSRPQPNMEVISKLKPDLIIADVSRHK 123
9 VVFMLILVVAVAGGGQKDT----EBKTEMTTIKDELGTEKIKGNPKRIVVLEYSFADYL 63
                                                                                                                                                                                                                                                                                                     244 NEELANINPKVMILATNGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKMLQSR
                                                                                                                                                                                                                                                      VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK
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                                                                                                                                                                                                                                                                                                                                          13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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                                                                                                                                                                                             11;
                                                                                                                                                                            DB 2; Length 319;
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168;
MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                         42.6%; Score 719.5; DB 2;
46.2%; Pred. No. 1.2e-31;
tive 65; Mismatches 95;
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Name=yfmC; OrderedLocusNames=BSU07520;
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                          311 GLISSEEMAKELVELSKK 328
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GIMASESMAEDLEKIAEK 317
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                     Best Local Similarity 46.2
Matches 147; Conservative
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WEDLINE=97417488; PubMed=9272861; DOI=10.1016/80378-1119(97)00130-3;
WA Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
Toloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three apore germination proteins, an iron uptake system and a general stress response protein.";
Gene 194:139-199(1997).
BEMBL; 299108; CAB12581.1; -.
REMBL; 299108; CAB12581.1; -.
REMBL; 299108; CAB12581.1; -.
REMBL; 299108; CAB12581.1; -.
REMBL; D86417; BAA22317.1; -.
REMBL; CO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
Remple: Proteins Remple: 
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Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
Medique C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
A Medique C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
A Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
A Presort A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,
Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
A Shin B.S., Soldo B., Sorokin A., Taroconi E., Tarbanashi H.,
Takemaru K., Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P.,
Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
Yasumoto K., Yata K., Yoshikaw H.P., Zumstein E.,
Mella M., Mandella M., Yamame M., Mandella M.
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"The complete genome sequence of the Gram-positive bacterium Bacillus
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Query Match
Best Local Similarity
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R. Perscott A., Wandler E., Wandenbol M., Yannier F., Wannerder S., Wedlikawa H., Danchina A.;

R. Weltzenegger T., Winters P., Wipat A., Yamamotch H., Yamane K., Yashingawa H., Danchina A.;

R. Phile Complete genome sequence of the Gram-positive bacterium Bacillus
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GO; GO:000627; P:high affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla BP.
Pfan; PP0197; Peripla BP 2; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 348 AA; 38551 MW. EBT.
                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                          Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                             Last sequence update)
Last annotation update)
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41.2%; Pred. No. 1.1e-25;
                                                                            Hypothetical protein yhfQ.
Name=yhfQ; OrderedLocusNames=BSU10330;
Bacillus subtilis.
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PRT;
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PRELIMINARY;
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                                                                                                                                       NCBI_TaxID=1423;
               O07616; Q796T6;
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                                                             204
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; Pred. No. 1.4e-25;
69; Mismatches 118; Indels 7
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Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.;
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
YhfQ (Aminotransferase, Class-II).
Name-yhfQ; ORFNames=BL01086, BLi01111;
Bacillus licheniformis DSM 13.
Bacillus Frmicutes; Bacillales; Bacillus.
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EMBL, CP000002; AAU2571.1; -.
Aninotransferase; Transferase.
SEQUENCE 325 AA; 35892 MW; 031DD170751A0577 CRC64;
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181 KQKFG-SRKQSILLLLGNTNEEITVRDENFFTSQLLTKIGYTYGVGDS-GKGDAENGESVN 238
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                                                                 201 VEVLGYQMPKARADN-----QPNASVGLEQVAAEKPDLMILIHYR---DESIARK
                                           LOMNTETLSQVNPERMFIMT-NKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWA
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MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;

MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

MCOMplete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL., AE0066047; ARX02215.1;

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006827; Pihigh affinity iron ion transport; IEA.

InterPro; IRR002491; Peripla BP.

Pfam, PP01497; Peripla BP.2; I.

COMplete protecome.

SEQUENCE 298 AA; 32954 MW; 55C1CA6834F1C490 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                               Name=fecB; OrderedLocusNames=PM0131;
Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellacea; Pasteurella.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ferric vibrioferrin-binding periplasmic protein PvuB.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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225 QLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSL-KELEK 283
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STRAIN=RIMD 2210633 / Serotype O3:KG;
STRAIN=RIMD 2210633 / Serotype O3:KG;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;
MREDLINE=225084654; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;
Makino K., Oshima M., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.",
Lancet 361:743-749(2003).
BMBL; Ap005089; BAGC5998:1; ---
GO; GO:000581; F:iron ion transporter activity; IEA.
GO; GO:0006827; F:high affinity iron ion transport; IEA.
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Vibrio parahaemolyticus.
Batceria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBL_TaxID=670;
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EMBL, AB082122; BAC16540.1; --

GO, GO:0006821; F:iron ion transporter activity; IEA.

GO; GO:0006827; P:high affinity iron ion transport; IEA.

InterPro; IPR003491; Peripla BP.

Pfam; PF01497; Peripla BP.2; 1.

SEQUENCE 307 AA; 34309 FW; F6D94659A46245A7 CRC64;
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Tanabe T., Funahashi T., Nakao H., Miyoshi S., Shinoda
Yamamoto S.;
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Best Local Similarity 36.24
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TQETIQPGVVSDKGMMLHSPVSYAGGVLSTLGIQSPLAPSE-----RNAYIPTSFEL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSQVNPERMFIMTNKASSNEPSL-KELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLIS 314
                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                        196 KNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTET
                                                                                                                                                                                                                                                                    16 LLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVAL
                                                                                                                                                                                                                                                                                                                                                                                     DVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Mismatches 107; Indels 14; Gaps
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photorhabdus luminescens (subsp. laumondii).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                                                                                                                                                                                            23;
                                                                                                                                                      DB 2; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 302;
                                                                                                                                                                                                            Indels
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                                                                                                 DDA125C81E0E1638 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1ron(III) dicitrate-binding periplasmic protein FecB.
Name=fecB; OrderedLocusNames=plu4447;
                                                                                                                                                      28.8%; Score 487.5; DB 2; 35.4%; Pred. No. 5.1e-19; ive 72; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 476; DB 2; 36.0%; Pred. No. 2.1e-18;
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Nat. Biotechnol. 21:1307-1313(2003).
EMBL; BX571873; CAE16819.1; -.
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           InterPro; IPR002491; Peripla_BP
                                      Pfam; PF01497; Peripla_BP_2; 1.
                                                                                                 34185 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                               Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AEEIARNLEAL 303
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Best Local Similarity
                                                                                                 307 AA;
                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=141679;
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                                                                                                    SEQUENCE
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Q7MZ5

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103 TSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK 162
                                         163 TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGOF 222
                                                                                                                                                                          223 ISQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE 282
                                                                                                                                                                                                                                                                                                           41 DGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIG
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PubMed=15263089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Bell K.S., Sebaihia M.R., Bentley S.D., Churcher L.J.C., Mungall K ,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H ,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S ,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.,
"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=fecB, OrderedLocusNames-ECA1076;
Brwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum)
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 FKTISKALGKEEEGKKRLEEHDKKIEEYKKEITWDKNOKVLPAVAAKSGLLAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
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                                                                                                                                                                                                                                                                                                                                                                                                            KDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODTLWOMMTAOHKHOIAAVDSNTWARMRGIFAAERIGSDAVKI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).

EMBL, BX950851; CAG73987.1; -
GO, GO:0005381; Firon ion transporter activity; IEA.
GO; GO:0006537; P:high affinity iron ion transport; IEA.
InterPro; IPR002491; Peripla_BP.
Pfam; PP01497; Peripla_BP_2; 1.
Complete proteome.
SEQUENCE 304 AA; 31394 MW; A280B695134CCBA5 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Iron(III) dicitrate-binding periplasmic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AA
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SVLAALGL-----SVPKPIN---NAPMASINLEQLLAINPOWLIVTHYR---EESIVKR 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 GEMVGKKREMQARLEQHKERMAQWASQ--LPKGTRVAFGTSREQQFNLHTQETWTGSVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                         DOI=10.1128/IAI.69.10.6012-6021.2001,
Luck S.N., Turner S.A., Rajakumar K., Sakellaris H., Adler B.;
"Ferric dicitrate transport system (Fec) of Shigella flexneri 2a
YSH600 is encoded on a novel pathogenicity island carrying multiple
antibiotic resistance genes.";
Infect. Immun. 69:6012-6021(2001).
                                                                                                                                                                                                                                                                                           Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                LEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVELSK 327
                                                    Length 300;
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ID FECB ECOLI

AC P15028; P76816;

DT 01-AP1990 (Rel. 14, Created)

DT 10-OCT--2003 (Rel. 42, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DT 25-JAN-1005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
InterPro; IPRO491; Peripla BP.
Pfam; PPO1497; Peripla BP. 2; 1.
SEQUENCE 300 AA; 33166 WW; 6E0B0CF5B99AAAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luck S.N., Turner S.A., Rajakumar K.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF326777, AAL08454.1; -
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                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                        2
                                                                                                                                                                                         Created)
                                                                                                                                                     PRT;
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                                                                                                                                                                                   (TrEMBLrel. 19, (TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                        Shigella flexneri 2a.
Bacteria, Proteobacteria, Gan
Enterobacteriaceae, Shigella.
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                                                                                                                                                      PRELIMINARY;
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01-DEC-2001
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS 224
                                                                                                                                                                                                                                                                                                                                    "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119 (1995).
-!- FUNCTION: Binds citrate-dependent iron(III); part of the binding-protein-dependent transport system for uptake of citrate-dependent
                                                                                             THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 VQDEHGTFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 IKHEBGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Belongs to the bacterial extracellular solute-binding
                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Iron(III) dicitrate-binding periplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein family 8.
SIMILARITY: Contains 1 iron siderophore/cobalamin periplasmic-binding domain.
                                                             Nerve
                                                                                                                      147
                                  SSEATTG
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SSWEPSLIKE 280
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                                                                                                                                                                                                                                                                               STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                           Standenmaier H., van Hove B., Yaraghi Z., Braun V., "Nucleotide sequences of the feeBCDE genes and locat. proteins suggest a periplasmic-binding-protein-dependen. mechanism for iron [III] dicitrate in Escherichia coli."; J. Bacteriol. 171:2626-2633(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fe/B12 periplasmic-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 Fe/B12 periplasmic-binding
8 L -> V (in strain B).
23 T -> M (in Ref. 1).
57 I -> S (in Ref. 1).
33146 MW; 6024ED0F9C82D0EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.2%; Score 460; DB 1; 35.5%; Pred. No. 1.6e-17;
                                                             Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacte?
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                            Periplasmic
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EMBL; U00096; AAC77246.1; ALT_INIT.
PIR, S56515; QRECD3.
ECOGENE; EB0283; --
ECOGENE; EQ10287; fecB.
                                                 Name=fecB; OrderedLocusNames=b4290;
                                                                                                                                                 STRAIN=K12;
MEDLINE=89213950; PubMed=2651410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002491; Peripla BP. Pfam; PF01497; Peripla BP 2; 1. PROSITE; PS50983; FE BI2 PBP; 1.
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SIMILARITY: Belongs to
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                                                                                                                                    SEQUENCE FROM N.A.
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23
53
                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                         Blattner F.R.;
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 NRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 GRHOALYNDLASLAPTLMLPSRGEDYQGSLKSAGLIGMALGKGPEMQARIAENRQHLKTV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LOVPE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 LOMNTETLSQVNPERMFIMTNK----ASSNEPSLKEL-EKDPVWKKLNAVKNQRVDILDR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLGPKEALSDDVTKGLSKYLKGPYL-QMNTETLSQVNPERMFIMTNKASSNEPSLKELEK 283
GEMVGKKREMOARLEOHKERMAOWASO--LPKGTRVAFGTSREOOFNLHTOETWTGSVLA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Iron(III) dicitrate transport system, periplasmic iron-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKV--PKHPKRVVVLEYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLACGLL-TLLASAA------OAAPIDIDDGOHKVHLPDTPKRVVVLEFSF
                                         202 SLGL------NVPAAMAGASMPSIGLEQLLAVNPAWLLVAHYR---EESIVKRWOO
                                                                                                                                                                                                                                                                                                                                                                                     Muchall C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zarar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Bender C.L., White O., Fraser C.M., Collmer A.;

The complete genome sequence of the Arabidopsis and tomato pathogen Proc. Natl. Acad. Sci. US.A. 100:10181-10186 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                                                STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
                                                                                                                                                                                                                                                                                  Рвеидотопав вугіпдае (рv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Рвеидотопадаlев.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005381; F:iron ion transporter activity; IEA. GO; GO:0006827; P:high affinity iron ion transport; IEA. InterPro; IPR002491; Peripla_BP. PF6m; PF01497; Peripla_BP_2; 1.
                                                                                          249 DPLWQMLTAAQKQQVASVDSNTWARMRGIFAAERIAADTVKI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 AA; 32872 MW; 371BA711BC7A6108 CRC64;
                                                                             DPVWKKLNAVKNORVDILDRDLWARSRGLISSBEMAKELVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.9%; Score 454.5; DB 2 34.6%; Pred. No. 3.2e-17;
                                                                                                                                                                                                                                                                    Name=fecB; OrderedLocusNames=PSPTO0763;
                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                            Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.9%;
Best Local Similarity 34.6%;
Matches 112; Conservative 6
                                                                                                                                                                        PRELIMINARY;
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SEQUENCE 306 AA
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01-OCT-2003
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DVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE-----KDPVW 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-K77(2004).

EMBL; AE017333; AAU443302.1; -.

EMBL; CP0000002; AAU24933.1; -.

SEQUENCE 325 AA; 36700 MW; 949283E3C6C24775 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LKILSVIGLLFVLIAT -- AACGNNSSSNSSKESSKDGVEIKHEEGT - TKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
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В.В.
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Rey M.W., Ramalya P., Nelson B.A., Brody-Karpin S.D., Zaretsky Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 325;
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                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                           (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.6%; Score 415.5; DB 2; 33.2%; Pred. No. 4.6e-15; ive 63; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Veith B., Herzberg C., Steckel S., Feesche J.,
Ehrenreich P., Baeumer S., Henne A., Liesegang
Ehrenreich A., Gottschalk G.,
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                                                                                                                                                                                                                                                                                                             YfiY (Periplasmic binding protein).
Name=yfiY; ORFNames=BL02129, BLi03475;
Bacillus licheniformis DSM 13.
                        | |||:||:||::||
| DSWARNRGIMASEQIADDALAVLK 298
DLWARSRGLISSEEMAKELVELSK .327
                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15383718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM 13;
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25-OCT-2004
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Query Match
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Q7A2Y7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOFLSOLGFKEALSDDVTKGL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.8%; Pred. No. 1.7e-14;
Nes 113; Conservative 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

PubMed=14688077; DOI=10.1128/IAI.72.1.29-37.2004;

PubMed=14688077; DOI=10.1128/IAI.72.1.29-37.2004;

Bale S.E., Doherty-Kirby A., Lajoie G., Heinrichs D.E.;

"Role of siderophore biosynthesis in virulence of Staphylococcus "Role of siderophore biosynthesis in virulence of Staphylococcus aureus: identification and characterization of genes involved in
                                                                                                                                                                                                                                                                                                                            Heinrichs J.H., Gatlin L.E., Kunsch C., Choi G.H., Hanson M.S., "Identification and characterization of SirA, an iron-regulated protein from Staphylococcus aureus."; J. Bacteriol. 181:1436-1443(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 330;
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                                                                                       Last sequence update)
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Last annotation update)
                                                                                                                                                                              Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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EMBL; AF079518; AAC62496.1; -.
EMBL; AY251022; AAP82062.1; -.
                                                             01-NOV-1998 (TERMBLrel. 08, 01-NOV-1998 (TERMBLrel. 08, 25-OCT-2004 (TERMBLrel. 28, Lipoprotein SirA.
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05-JUL-2004
05-JUL-2004
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SEQUENCE 3
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Q7A1Z7
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                                                                                                                                                                                   MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagabi Y., Imama N., Asano K., Naimi T., Kuroda H., Cui L., Yamanoto K., Hiramatsu K., Hiramatsu K., Hiramatsu K., Agenome and virulence determinants of high virulence community-
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EMBL, AP004822; BAB93953.1; GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IEA.
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SEQUENCE 330 AA; 36744 MW; 63710BA22B208F61 CRC64;
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Staphylococcus aureus (strain MuSO / ATCC 700699).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                   Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Matches 113; Conservative
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5 IKML-VVTLAFLLV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYQG
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                                                                                                                                                                MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai V., Lian J.-Q., Ito T., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanenisa M., Vamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                 8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
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                                                                                               Length 330;
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    Lancet 357:1225-1240(2001).
EMBL, AAD003358; BABS6277.1; -.
GO, GO:000581; Filton ion transporter activity; IEA.
GO, GO:0006827; P:high affinity iron ion transport; IEA.
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                                                         Complete proteome; Lipoprotein.
SEQUENCE 330 AA; 36744 MW; 63710BA22B208F61 CRC64;
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                                                                                            Query Match

24.0%; Score 405; DB 2;
Best Local Similarity 32.8%; Pred. No. 1.7e-14;
Matches 113; Conservative 65; Mismatches 132
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Name-sirA; OrderedLocusNames-SA0111;
Staphylococcus aureus (strain N315).
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Matches 113; Conservative
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SEQUENCE 330 AA
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LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS

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68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD 127
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Subjuance From. No. 19.

PubMed=1521324; DO: 10.1073/pnas.0402521101;

A Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,

A Baright M.C., Footer T.J., Moore C.E., Hurst L., Atkin R.,

Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,

A Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,

A Peltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,

A James K.D., Lennard N., Line A., Mayes R., Moule S., Murgall K.,

Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,

Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J.; Revens K., Whitehead S., Barrell B.G.,

Spratt B.G., Parkhill J., Colinical Staphylococcus aureus strains:

"Complete genomes of two clinical Staphylococcus and drug resistance.";

T. evidence for the rapid evolution of virulence and drug resistance.";

Proc. Natl Acad. Sci. U.S.A. 101:9786-9791(2004).

BMBL; BX571857; CAG41856.1;

CO; GO:0005381; Fiiron ion transporter activity; IEA.

BREPTO; PRENO02491; Peripla BP. 2: 1.

Reference of the stable and a ffinity iron ion transport; IEA.

Reference of the stable BP. 2: 1.
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FVDALVALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLIIAD
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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Best Local Similarity 32.8
Matches 113; Conservative
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              Holden M.T.G., Feell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Raright M.C., Foeter T.J., Moore C.E., Hurst L., Akkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Charles K.D., Lennard N., Line A., Mayes R., Moules S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Mungall K.,
James R.D., Simmonds M., Stevens K., Whitehead S., Mungall K.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.;
Tomplete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
R. M. Starbell F. Firon ion transporter activity; IEA.

GO: GO:0005891; Firon ion transporter activity; IEA.

R. Pelley, Peripla B.P. 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ATDVAVSLGVKPVGAVESWTQKPKPEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 QKQVDNGKDIIQLTSKESIPLMNADHIFVVKSDPNAKDAALVKKTESEWTSSKEWKNLDA 288
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                                                 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA
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32.8%; Pred. No. 1.7e-14;
ive 65; Mismatches 132; Indels 34; Gaps
                                                                                                                289 VKONQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                  293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 AA; 36717 MW; F815203503849D6D CRC64;
                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                             NamesirA, OrderedLocusNames=SAR0118;
Staphylococcus aureus (strain MRSA252).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
MCBI_TaxID=282458;
                                                                                                                                                                                                                                                                                                                                             PubMed=15213324; DOI=10.1073/pnas.0402521101;
                                                                                                                                                                                        330 AA
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Matches 113, Conservative
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72 LVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRH 131
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SEQUENCE FROM N.A.

STRAIN=Amee / isolate Porton;

Read T.D., Peterson S.W., Baillie L.W., Paulsen I.T.,

Read T.D., Peterson S.W., Elsen J.A., Gill S.R.,

Rolonay 'J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

Rolonay 'J.F., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Ranton J.L., Mahamoud Y., Jiang L., Hance I.R., Neldman J.F.,

Barty K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nietman W.C.,

Razberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

Closely related bacteria.";
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.;
Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 VFSLAFSIL-LSACGKSNTKEESKEDTKKEMIPVEHAMGKTEVPANPKRVVILTNEGTEA
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EMBL, AE017026; AAP224632.1; --

EMBL, AE017334; AAT29716.1; --
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                                                                                                                                                                                                                                                                                    081V85; Q613H2; Q6KX85; 01-UN-2003 (TEMBLEE). 24, Created) 01-UN-2003 (TEMBLEE). 24, Last sequence update) 01-CUN-2003 (TEMBLEE). 28, Last annotation update) 15-OCT-2004 (TEMBLEE). 28, Last annotation update) 1ron compound ABC transporter, iron compound-binding protein. OrderedLocusNames=BA0615, BAS0581, GBAA0615;
                                          289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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TIGR; BA0615; -.
GO; GAA0615; -.
GO; GO:0005815; Fixon ion transporter activity; IEA.
GO; GO:0006827; Pinigh affinity iron ion transport; IEA.
GO; GO:0005817; Pinigh affinity iron ion transport; IEA.
Fran; PPE01497; Peripla_BP.
Complete proteome.
SEQUENCE 321 AA; 36302 MW; BB17CFF136D893CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI_TaxID=1392;
293 VICNORV-DILDRDLWARSRGLISSEBMAKELVELSKKDSKKUNK
                                                                                                                                                                                                                                                                 321 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus anthracis.
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NCBI_TaxID=222523;
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25-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 YKOLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEBYKKEITM 194
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                                                                                                                                                                                                                                                         248 YLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEK----DPVWKKLNAVKNQRVDILDR 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 ILAPSLILSACGKSNTKEESKEDTKKEMIPVEHAMGKTEVPANPKRVVILTNEGTEALLE 74
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kinaka R.,
                                        : ||:: : ::| | : ::| | : :| | CDKVNQEISMVRFMPGDVRIYHGDTFSGVILKELGFKRPGDQNKNDFAERNVSK----
                                                                                                                                                                                                                                                                                           192 KVNQEISMVRFMPGDVRIYHGDTFSGVILKELGFKRPGDQNKDDFAERNVSK-----
KGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKE
                                                                                                                            ITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGP
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K. Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K. Hitchrock P., Jackson P., Tice H.;
Richardson P., Rubin B., Tice H.;
"Complete genome sequence of Bacillus thuringiensis 97-27.";
"Complete genome sequence of Bacillus thuringiensis 97-27.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017355, AAT62409.1;
GO; GO:0005381; Firon ion transporter activity; IEA.
GO; GO:0005827; P:high affinity iron ion transport; IEA.
InterPro; IRR002491; Peripla BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last aequence update)
1ron(III) dicitrate ABC transporter, periplasmic protein.
Name=fecB; OrderedLocusNames=BT9727_0525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.9%; Score 404; DB 2; Length 32
.larity 31.4%; Pred. No. 1.9e-14;
Conservative 73; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp. konkūkian).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=180856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 AA; 36373 MW; 47F614F471C1CFF3 CRC64;
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NTAGGVMAANLLLDDIEKRFVK 321
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Q6HNJ9
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75 LGVKPVGAVKSWTGDPWYPHIKDKMKDVKVVGDEGQVNVETIASLKPDLIIGNKMRHEKV 134
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PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A.; Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Rasko D.A.; Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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, Okinaka
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Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C.,

Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., (
Richardson P., Rubin B., Bacillus cereus ZK.";

"Complete genome sequence of Bacillus cereus ZK.";

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CP000001; AAU19716.1;

SEQUENCE 321 AA; 36315 MW; OAIB4742BlAB7945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
23.6%; Score 399; DB 2; Length 32
Best Local Similarity 31.4%; Pred. No. 3.6e-14;
Matches 101; Conservative 71; Mismatches 122; Indels
                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TREMBLRel. 28, Last annotation update)
Tron(III) dicitrate ABC transporter, periplasmic protein.
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NCBI_TaxID=288681;
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Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus
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Last annotation update)
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321 AA
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(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 NTAGGVMAANLLLDDIEKRFVK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                               Name=fecB; ORFNames=BTZK0525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus cereus ZK.
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Matches

Query Match

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                                                                                                                                                                                                                                                                                        194 MDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGPYL 249
                                                                                                                                                                                                                                                                                                                                                                        250 QMNTETLSQVNPERMFIMTNKASSNEPSLKELEK----DPVWKKLNAVKNQRVDILDRDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                ----ERISAMDGDVLFYFTFD-KGNEKKGSELEKEYINDPLFKNLNAVKNGKAYKVDDVI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKOPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PDLIIADNNRHKGIYKDLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                            74 ALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKG 133
                                                                                                                                                     75 ELGUKPUGAVKSWTGDPWYPHIKDKWKDVKVVGDEGQVNVETIASLKPDLIIGNKWRHEK 134
                                                                                                                                                                                                            134 IYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEIT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                              73
                                                                                    74
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                                                                                                                                                                                                                                 192 DKVNQEISMVRFMPGDVRIYHGDTFSGVILKELGFKRPGDQNKDDFAERNVSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KILSI----FIVVLLFAVGCGQQKEBKKETKADNKNQAITIKHAEGETKLDKPAKKVVVL
                                            16 LLFVLIATAACG---NNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALV
                                                                     9 KILSVIGILFVLIATAACGNNSSSNSSKESSKD----GVEIKHEEGTTKVPKHPKRVVVL
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        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorotha, Anderson I., Galleron N., Candelon B.,
Rapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Bhrlich S.D.,
Overbeek R., Kyrpides N.C.;
"Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 392; DB 2; Length 324; larity 34.4%; Pred. No. 8.7e-14; Conservative 59; Mismatches 122; Indels
        73; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=BC4528;
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteilus (Firmitutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AA; 36040 MW; 884FC3950A0553A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 WNTAGGVIAANLLLDDIEKRFVK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 WARSRGLISS ---- EEMAKELVE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01497; Peripla BP 2; 1
PRINTS; PR01715; FERRIBNDNGPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrichrome-binding protein.
        Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=226900;
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                                                                                                                                                                                                                                                                                                                                                                                                                  245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q817L3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                      195 DKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKYLKGPYLQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 MNTETLSQVNPERMFIMT-NKASSNEPSLKELEK----DPVWKKLNAVKNQRVDILDRDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ERISAMDGDVLFYFTFDKGNENKGS--ELEKEYINDPLFKNLNAVKNGKAYKVDDVI 298
                                                                                                                                                                                                                                                                                                                                                                                               LDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITM 194
                                                                                                                                                                                                                                                                                                                                      adaptations and a large plasmid related to Bacillus anthracis pXOl.";

Nucleic Acids Res. 32:977-988(2004).

BMBL; AE017066; AAS39616.1;

TIGR; BCE0663;

GO; GO:0005381; F:iron ion transporter activity; IEA.

GO; GO:0006381; Peripla affinity iron ion transport; IEA.

Interbro; IPR002491; Peripla BP.

Pfam; PF01497; Peripla BP.2; 1.
                                                                                                                                                                                                                                                                                                               16 LLFVLIATAACGNNSSSNSSKE-SSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhatcacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                       30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 322;
                                                                                                                                                                                                                                 Length 321;
                                                                                                                                                                                                                             23.5%; Score 397; DB 2; Length 32: 31.0%; Pred. No. 4.6e-14; tive 77; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mature AZONO AAPO7634.1; -- BMB, AZONO AAPO7634.1; -- GO, GO:0005381; F: Iron ion transporter activity; IEA. GO; GO:0006827; P: high affinity iron ion transport; IEA. THEATORY: IPR002491; Peripla BP.
                                                                                                                                                                                       321 AA; 36322 MW; ACDEA9056A566FA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA; 36417 MW; 760088C3D5D6E9FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24, Last sequence update) 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.5%; Score 396.5; DB 2 31.0%; Pred. No. 4.9e-14;
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Iron(III) dicitrate-binding protein.
OrderedLocusNames=BC0616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 WARSRGLISS ---- EEMAKELVE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNTAGGVMAANLLLDDIEKRFVK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF01497, Peripla BF
Complete proteome.
SEQUENCE 322 AA.
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                    Complete proteome
SEQUENCE 321 AA
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01-JUN-2003

RESULT 34
081109
070110
AC 081110
DT 01-JT
DT 01

981109

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GAEALLAVGVTPVGTTKPRAGDEWYPHLAKELKNTEVVGTERDINLEAVMKLKPDLIIGN 124
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KILSVIGLLFVLIATAACG-NNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 MXEKIGDKINSKVSIIRFVPGDVRIYQKNSFSGVVINDIGFKRPPLQDKDDFAIKGIIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKGPYLQMNTETLSQVNPERMFIMT-----NKASSNEPSLKELEKDPVWKKLNAVKNQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFK----EALSDDVTKGLSKY
                                                                                   175 LADMDKAFADAKAKIEKADLKDKNIAMAQAFTAKNVPTFRILT--DNSLALQVTKKLG--
                                                                                                                             EALSDDVTKGLSKYLKGPYLOMNTETLSQVNPER-MPIMTNKASSNEPSLKELEKDPVWK
                                                       178 LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kapatral V., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Bhrlich S.D., Overbeek R., Kyrpides N.C., Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Match 23.1%; Score 391; DB 2; Length 32
Local Similarity 30.2%; Pred. No. 9.7e-14;
Les 98; Conservative 64; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0005381; F:iron ion transporter activity, IEA. GO; GO:0006827; P:high affinity iron ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA; 36173 MW; 95ED63B62B07323F CRC64;
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Iron(III) dicitrate-binding protein.
                                                                                                                                                                                                     289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                            284 ELKPKKENKMYKLKGDTWIFG-GPESATSLATQVADV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DILDRDLWARSRGLISSEEMAKEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 FQVDEVIWNTAGGIKAANLMLDDI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE017005; AAP09174.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=BC2208;
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 423:87-91(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
SEQUENCE 320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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1081DY
AC Q81DY
AC Q81DY
DT 01-JUI
DE IVAN
REDULII
RA KAPAT
RA KAPAT
RA KAPAT
RA IVANO
RA Grech
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65 EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKOPNLEEISKLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Ames / isolate Porton;

X MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

A Rolonay J.F., Beanan M.J., Dodson R.J., Brinker D.M., Wu M.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Mahamoud Y., Jiang L., Hakins K.L., Nierman W.C.,

Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

A slaberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

T. The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Federova N.B.,
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin B., Tice H.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AR017038; AAP28458.1; -.
EMBL; AR017334; AAT33889.1; -.
IIGR; BA4766; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                     081L65; Q6HSL7; O6KLM1;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Iron compound ABC transporter, iron compound-binding protein.
OrderedLocusNames=BA4766, BAS4424, GBAA4766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR002491; Periplame.
                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae;
324 AA
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PRINTS; PR01715; FERRIBNDNGPP
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Matches 116; Conservative
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                                                                                                                                                                                                                                          Bacillus anthracis.
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NCBI_TaxID=279010;
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                                                                           LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                    230 EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richhardson P., Rubin E., Tice H.;

Richhardson P., Rubin E., Tice H.;

"Complete genome sequence (E Bacillus thuringiensis 97-27.";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ABC11355, AAT60882.1;

GO; GO:0005381; Firon ion transporter activity; IEA.

GO; GO:0005381; Pinon ion transporter activity; IEA.

InterPro; IPR008091; Perfitnity iron ion transport; IEA.

InterPro; IPR008091; Perfitnity iron ion transport; IEA.

InterPro; IPR00491; Peripla BP.

PÉRM: PR01497; Peripla BP. 2; 1.

PRINTS; PR01715; PERRIBNNGPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iron compound ABC transporter, iron compound-binding protein.
Name=fhub; OrderedLocusNames=187977_4264;
Bacillus thuringlensis (subsp. konkukian).
NCBI_TaxIb=180856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TremBirel. 27, Last sequence update) (TrEMBirel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                           :| :: : : : : : ELKFKKENKMYKLKGDTWIFG-GPESATSLATQVADV 319
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                                                                                                                                                                                                                                                              KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
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05-JUL-2004
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EMBL; AE017333; AEU34242.1; -.
EMBL; CP0000002; AAU22065.1; -.
SEQUENCE 315 AA; 34672 MW; E239649B55EB47DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zaretsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC 14580, Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky Rey M.W., Ramaiya P., Xiang H., Gusti V., Clausen I.G., Olsen Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 315;
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Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.
Ehrenreich A., Gottschalk G.;
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                                                                                                                                                                                                                                         Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
                                                    25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
YClQ (Periplasmic binding protein).
Name=yClQ; ORRNames=BL01760, BLi00466;
Bacillus licheniformis DSM 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.5%; Score 380; DB 2; I 32.8%; Pred. No. 3.8e-13; Live 64; Mismatches 129;
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25-OCT-2004 (TrEMBLrel. 28, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 IIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 KIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGF---KEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 SKYLKGPYLQMNTETLSQVNPERMFIMT-----NKASSNEPSLKELEKDPVWKKLNAVKN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VRGLKILSVIGLLFVLIATAACGNNSSSNSS-KESSKDGVEIKHEEGTTKVPKHPKRVVV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).

GENBL; AE017333; AAU42478.1; -.

EMBL; CP0000002; AAU25109.1; -.

Hypotherical protein.

SEQUENCE 315 AA; 34861 MW; F018C0B904038C96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Gaps
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Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
                                                                                                                                                                                          Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G., "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 315;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Periplasmic binding protein).
ORFNames=BL03470, BLi03657;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=279010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.5%; Score 379.5; DB 2; 29.7%; Pred. No. 4e-13; tive 70; Mismatches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNVHKVSDAIWNTAGGVLAANLMLDDI 309
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Job time : 71 secs
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Best Local Similarity 29.7%
Matches 97; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2005, 09:19:06; Search time 20 Seconds (without alignments) 1611.631 Million cell updates/sec Run on:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	l	hypothetical prote	ferrichrome ABC tr	iron(III) dicitrat	citrate-dependent	lipoprotein [impor		$\vdash$	Ψ	î		_	_	_		iron(III) dicitrat	periplasmic iron-c	hypothetical prote	iron(III) dicitrat	iron(III) dicitrat	Ē		iron(III) dicitrat	iron-uptake system	Ħ	_		_	iron(III) dicitrat
ID	D90013	E89872	B69812	F69831	QRECD3	G89771		E83779	E69763	G84123	AH2128	AG2082	AG2129	S74458	AC2421:	AF2082	AC1855	A89846	AD2134	AD2082	AE2074	AD2085	AD2079	I39842	S32930	AG2075	T36412	AB2130	A11943
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Length	327	319	315	348	302	330	325	341	317	334	328	325	330	330	319	326	300	342	331	330	361	319	357	317	315	343	350	333	331
* Query Match	72.9	42.9	40.2	36.2	27.2	24.0	22.1	20.7	19.7	19.7	19.3	18.3	17.5	17.3	17.1	17.0	16.9	16.9	16.8	16.5	16.4	16.4	16.4	16.4	16.3	16.2	16.2	16.2	15.8
Score	1232	724.5	679.5	611	460	405	373	350	332.5	332.5	327	310	295.5	292.5	288.5	288	285	285	284	279.5	278	277.5	277.5	276.5	275	274	274	273	267.5
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RESULT

hypothetical prote ferrichrome bindin	ABC transporter (b enterochelin uptak iron(III) dicitrat	hypothetical prote hypothetical prote	hypothetical prote hypothetical prote	hypothetical prote B. subtilis ferric ABC transporter, s	conserved hypothet iron(III) dicitrat ferrichrome bindin
B86666 AG1319	D70074 H81279 S74441	B95119 F97988	AF2130 G95218 E98082	D83778 AG1378 AG2880	G97656 AB2078 AG1691
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265 264.5	261.5	254	254 253 253	250.5 249.5 246.5	246.5 242.5 240.5
30	332	933	337 387	4 4 4 0 1 2	44 44 5

## ALIGNMENTS

RESULT D90013 hypothe C;Speci C;Date: C;Acces R;Kurod ma, A;	RESULT 1 D90013 Dypothetical protein SA1979 [imported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus C.Species: Staphylococcus aureus C.Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C.Accession: D90013 R.Xuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
AjTitle AjRefer AjAcces AjStatu AjMoled	A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Aceseronce number: A89758; MUID:21311952; PMID:11418146 A;Accession: D90013 A;Accession: preliminary A;Actus: preliminary A;Actus: preliminary A;Actus: preliminary A;Actus: preliminary A;Actus: preliminary
A, Restances: A, Experimen C, Genetics: A, Gene: C, Superfami	A.Gross-references: UNIPROT:099589; GB:BA000018; PID:gl3701977; PIDN:BAB43269.1; GSPDB:C.A.Experimental source: strain N315 A.Experimental source: strain N315 A.Genetics: A.Genetics: C.Superfamily: ferrichrome-iron transport protein fecB
Query Ma Best Loc Matches	Query Match Best Local Similarity 71.9%; Score 1232; DB 2; Length 327; Best Local Similarity 71.9%; Pred. No. 2.6e-62; Matches 235; Conservative 42; Mismatches 50; Indels 0; Gaps 0;
& <del>4</del> 3	5 VRGLKILSVIGLIFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL 64 
& 8	65 EYSFVDALVALDVKPVGIADDNKKORIIKFLRDKIGKYTSVGTRKQPNLEEISKLKPDLI 124 
& <sup>8</sup>	125 IADNNRHKGIYKOLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGGKKRLEBHDKK 184    ::       :       :
& વ	185 IEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGGFLSQLGFKEALSDDYTKGLSKYL 244   :
& g	245 KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 304 [     ::    ::         :        :
o S	305 LWARSRGLISSEEMAKELVELSKKDSK 331 

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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C, Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 47.0%
Matches 149; Conservative
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                                                                    A;Molecule type: DNA
A;Residues: 1-315 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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B89872
hypothetical protein SA0891 [imported] - Staphylococcus aureus (strain N315)
C,Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89872
R;Kurcda, M: Ohta, T: Uchlyama, I:; Baba, T:; Yuzawa, H.; Kobayashi, I:; Cui, L.; Oguc
ma, A: Milautani-Ui, Y:; Kobayashi, N.; Sawano, T:; Inoue, R:; Kaito, C.; Sekimizu, K.;
C:; Shiba, T:; Hattori, M; Ogasawara, N:; Hayashi, H:; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89872
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 *KUR»
A;Residues: 1-319 *KUR»
A;Residues: 1-319 *KUR»
A;Cross-references: UNIPROT:Q99V55; GB:BA000018; PID:g13700840; PIDN:BAB42136.1; GSPDB:C
C;Genetics:
A;Gene: SA0891
C;Superfamily: ferrichrome-iron transport protein fecB
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C;Species: Bacillus subtilis
C;Species: Dacep1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B65812
R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Broon; B; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Nature 390
Nature 300
Natur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 NEELANINPKVMILATDGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AALDMKPVGIADDGSTKNITKSVRDKIGAYESVGSRPQPNMEVISKLKPDLIIADVSRHK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::||:::|| :: | | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | :: | | | :: | :: | | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIYKDLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
42.9%; Score 724.5; DB 2; Length 3
Best Local Similarity 46.9%; Pred. No. 8e-34;
Matches 149; Conservative 63; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:|| || ||::| ::::|
GIIASESMAEDLEKIAEK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
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iron(III) dicitrate-binding protein homolog yhfQ - Bacillus subtilis
CiSpecies: Bacillus subtilis
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterr
C.; Bron, S.; Broullet, S.; Bruschi, C.V.; Caddwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Enrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulgar, D.; Fritz, C.; Fullbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, S.; Hangela, S.; Haule, H.; Marchell, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schlach, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schlach, A.; Tamaka, T.; Tarpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A;Authors: Yoshikawa, H.F.; Zumaneton, E.; Yoshida, K.; Yata, K.; Yoshida, K.; Winters, P.; Wipat, A.; Tamaka, T.; Tarpetra, P.; Tognoni, A.; Tosato, V.; V.; Uchiyama, A;Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Athers preliminary, nucleic acid sequence not shown translation not shown
A;Cross-references: UNIPROT:034348; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12581.
A;Experimental source: strain 168
A;Experimental source: strain 168
A;Genteirs:
A;Genteirs: YfmC
C;Superfamily: iron(III) dicitrate transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: 007616; GB: 299109; GB: AL009126; NID: 92633260; PIDN: CAB12873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 FLDAVHNIGITPVGIADDNKKDMIKKLVGSSI-DYTSVGTRSEPNLEVISSLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 LKAELPKDENRNIVLGVARADSPQLHTSSSYDGEIFKMLGFTHAVKSD------NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 IAIMSVL-LLACLIVSGCSSSQNNNGSGKSESKDSRVIHDEEGKTTVSGTPKRVVVLELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEBISKLKPDLIIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEBGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 YLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWA
                                                                                                                                                                                                                                                                                                                                                                                                                           8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 YKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.2%; Score 611; DB 1; Length 348; 41.2%; Pred. No. 2.1e-27; ive 68; Mismatches 109; Indels 16;
                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                      40.2%; Score 679.5; DB 1; Length 315; 47.0%; Pred. No. 2.6e-31; Live 50; Mismatches 103; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: yhfQ
C; Superfamily: iron(III) dicitrate transport protein
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Gaps

224 203

164

104

85

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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 1.0-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89771
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:087491; GB:BA000018; PID:g13700031; PIDN:BAB41330.1; GSPDB:C. Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLGFKEALSDDVTKGLSKYLKGPYL-QMNTETLSQVNPERMFIMTNKASSNEPSLKELEK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNRHKGIYKDINKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SKYLKG--PYLOMNT-ETLSOVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A.Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAGEILINDLGFKR-----NKDL
                                                                                                                                                        VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII
                                                                                                                                                                                                                                                                                                                                                               SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                        VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                         45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Genetics:
A,Gene: BirA
C,Superfamily: Bacillus subtilis ferrichrome ABC transporter fhuD
      Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.0%; Score 405; DB 2; Length 330 32.8%; Pred. No. 7.3e-16; ive 65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoprotein [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 460; DB 1; L. L. L. S. S. S. S. Pred. No. 5.4e-19; Conservative 62; Mismatches 104;
                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.8%
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
Molecule type: DNA
Residues: 1-330 <KUR>
                                     Best Local Similarity
Matches 100; Conserv
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A;Status: prelimina:
A;Molecule type: DN
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            Query Match
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A; Title: The Complete genome sequence of Escherichia coli K-12. A; Reference number: S4720; MUD:97426617; PMID:9278503 A; Catus: nucleic acid sequence not shown; translation not shown A; Modecule type: DNA A; Reference number: A; Reference number: SEBA.
A; Resedues: 1-302 - SUB.A; A; R
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A;Accession: JS0112
A;Molecule type: DNA
A;Experimental source: strain K12
C;Comment: The sequence from strain B differs from that shown in having Val-10 and Thr-2
C;Comment: This protein is one of five, encoded by the fec operon, constituting a citrat
C;Genetics:
A;Gene: fec8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-302 < BLAT>
A; Residues: 1-302 < BLAT>
A; Croses-references: GB:AE000499; GB:U00096; NID:g1790732; PIDN:AAC77246.1; PID:g1790742;
A; Experimental source: strain K-12, substrain MG1655
B; Staudenmaier, H.; Van Hove, B.; Yaraghi, Z.; Braun, V.
B Bacteriol. 171, 2626-2633, 1989
A; Title: Nucleotide sequences of the fecBCDE genes and locations of the proteins suggest A; Reference number: PS0029; MUID:89213950; PMID:2651410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVNMKMTLEQLLKTDPDVIILMTGKTDDLDADGKRPIEKNVLWKKLKAVKNGHVYHVDR 320
                                                                                                                                                              127
                                                                                                                                                                                             187
                                           68
                                                                                                84
                                                                                                                                                                                                                                                                                                                TTRHKKYYDQLKKIAPTIALNNLNADYQDTIDASLTIAKAVGKEKEMEKKLTAHBEKLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                      205 TKQKISAN-SQSVLLIGNTNDTIMARDENFFTSRLLTQVGYRYAIS---TSGNSDSSNGG
                                           KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                          VDALVALDVKPVGIADDNKKNRII-KPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD
                                                                                                                                                                                                                                                                                 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIBE
                                                                                                                                                                                                                                                                                                                                                                                                          YKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSOLGFKEALSDDVTKGLSKYLKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- PYLOMNTETLSQVNPERMFIMTNKASSNEPSLKE-LEKDPVWKKLNAVKNQRVDILDR
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Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : | : : : | : | AVWSLRRSVDGANAILDELQKEMPAAKK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLWARSRGLISS----EEMAKELVELSK 327
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12;

67 62

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A;Residues: 1-341 <STO>
A;Cross-references: UNIPROT:Q9KE21; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A;Cross-references: UNIPROT:Q9KE21; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
C;Genetics:
A;Gene: BH1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LSVIGLLFVLIATAACGNNSSSNSS-----KESSKDGVE-----IKHEEGTTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%; Score 350; DB 2; Length 34
29.7%; Pred. No. 9.4e-13;
ive 63; Mismatches 138; Indels
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A; Reference number: A83650; MUID: 20512582; PMID: 11058132
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C, Superfamily: iron(III) dicitrate transport protein
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Pred. No. 8.2e-12;
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33.0%;
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Matches 102; Conservative
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                                                          A, Accession: E83779
A, Status: preliminary
A, Molecule type: DNA
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R.Kunet, F.; Ogsawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChG
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 290, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Lapidus, A.; Laudinois,
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
X.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
X.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
X.Authors: C.; Ogiwara, A.; Cudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Potalori,
X.Authors: Schleich, S.; Schroeter, F.; Roche, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Potalori,
X.; Muthors: Schleich, S.; Schroeter, H.; Yasumac, K.; Yasumoto, K.; Yasumoto, V.; Uchiyama,
T.; Winters, P.; Wippet, A.; Tammacoshi, H.; Panchin, A.; Tamakoshi, R.; Yasumoto, V.; Uchiyama,
T.; Winters, P.; Wippet, A.; Yamamoto, H.; Yasumoto, K.; Yasumoto, V.; Uchiyama,
A.; Reference number: A69580; MUID:98044033; PMID:9344377
A.; Reference number: A69580; MUID:98044033; PMID:9344377
A.; Reference number: A69580; MUID:98044033; PMID:9344377
A.; Restimental source: strain 168
C; Superfamily: iron(III) dicitrate transport protein
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ive 75; Mismatches 129; Indels
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iron(III) dicitrate-binding periplasmic protein [imported] - Nostoc sp. (strain PCC 712C 6;5pcies: Nostoc sp. PCC 7120 13.00 13.00 14.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 15.00 1
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A;Molecule type: DNA
A;Residues: 1-328 «KUR»
A;Cross-references: UNIPROT: Q8YTX0; GB: BA000019; PIDN: BAB74282.1; PID:g17131675; GSPDB:(
A;Experimental source: strain PCC 7120
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A,Note: Nostoc sp. Et 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C,Accession AG2082
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigucha Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy, Reference number: AB1807; MUID:21595285; PMID:11759840
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A,Residues: 1-325 «KUR»
A;Cross-references: UNIPROT:Q8YUW8; GB:BA000019; PIDN:BAB73912.1; PID:g17131304; GSPDB:C
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr2213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 YLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILD 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 FVDALVALDVKPVG---IADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.3%; Score 327; DB 2; Length 32
29.8%; Pred. No. 1.7e-11;
tive 71; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: alr2583
C;Superfamily: ferrichrome-iron transport protein fecB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 RDLWARSRGLISS----EEMAKELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 29.8
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Species: Older Species: Bacillus halodurans
C; Accession: G84123
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: G84123
A; Accession: G84123
A; Residues: 1-314 <STO>A; Residues: 1-314 <STO>A; Residues: 1-314 <STO>A; Cross-references: UNIPROT:Q9K6D8; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB075
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:||:|||||||| ||::| |::||||:
127 EIAKLQPDLIIASQLRHEEVYDQLSEIAPTV------VHETVFEFKETVELMGEAMDE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 GFK----EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGOF----LSQL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                    IEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOF--LSQLG----FKEALSDDVT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 JADVKK--TAEK-----LNKNGLVIMANDGKISAFGPKSRYGLIHDVFGVAPADONI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNE-PSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                       DNNRHKGIYKDLNKIAPTIELKSPDGDYNENI--DAPKTISKALGKEEEGKKRLEEHDKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFEFPENQKNSDEI-------FMLTDMESIPEMNADVFYMFMSDDETVQKTYEEWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 KASTHGGSVSY----EYISKTNPDYLFVIDRGTAIGETSSTKQVVENDYVKNVNAVKNG
                                                                                                   LLFVLIATA----ACGNNSSSNSSKESSKDGVEIKH--EEGTTKVPKHPKRVVVLEYSFV
                                                                                                                                                                                DAL -- VALDVKPVGIADDNKKNRIIKPL-RDKIGKYTSVGTRKQPNLEEISKLKPDLIIA
   Gaps
   41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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59; Mismatches 119; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVDILDRDLWARS-RGLISSEEMAKEL 322
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   Conservative
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A; Gene: BH3791
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      Matches
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67

Gaps

32;

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iron(III) dicitrate-binding periplasmic protein fecB-2a - Synechocystis sp. (strain PCC NyAlternate names: protein s1r1491 (Species: Synechocystis sp. (Species: Synechocystis sp. A;Variety: PCC 6803 (Species: Synechocystis sp. A;Variety: PCC 6803 (Species: Synechocystis sp. A;Variety: PCC 6803 (Species: 25-Apr-1997 #text_change 09-Jul-2004 (Spacession: S74458 (Spacession: Spimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996 (Spacession: Species) (Spacession: Spacession: Synechocystis A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-330 <KAN>
A;Cross-references: UNIPROT: P72610; EMBL: D90899; GB:AB001339; NID:g1651650; PIDN: BAA1661
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Accession: S74458
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                   292 SISAHNTNRIYFIDYQLASRIRGPIAAELFVNQVRQL 328
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28.4%; Pred. No. 1.5e-09;
tive 68; Mismatches 119;
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                                                                                                                              289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL
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243 K-LVSPESTE-
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A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Recession: AG3129
A;Reterence number: AB1807; MUID:21595285; PMID:11759840
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <a href="https://docs.org/no.com/">A;Residues: 1-330 <a href="https://docs.org/no.com/">A;Residues: 1-330 <a href="https://docs.org/">A;Residues: 1-330 <a 
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                                                                                         Length 325;
                                                                                         Query Match
18.3%; Score 310; DB 2; Length 32
Best Local Similarity 28.3%; Pred. No. 1.6e-10;
Matches 89; Conservative 71; Mismatches 124; Indels
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                C, Superfamily: ferrichrome-iron transport protein fecB
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2082
A;Accession: AF2082
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <KNR>
A;Residues: 1-226 <KNR>
A;Residues: 1-226 <KNR>
A;Coss.references: UNIPROT:QSYUW9; GB:BA000019; PIDN:BAB73911.1; PID:g17131303; GSPDB:C C;Genetics: alr2212
C;Superfamily: ferrichrome-iron transport protein fec8
A,Cross-references: UNIPROT:Q&YMLO, GB:BA000019; PIDN:BAB76622.1; PID:g17134061, GSPDB:d
A,Experimental source: strain PCC 7120
Genetical Source: strain PCC 7120
A,Gene: all4923
C,Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iron(III) dicitrate-binding periplasmic protein of ABC transporter alr2212 [imported] C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2082
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                                                                                                                                                                                                                                                                       VVLEYSFV-DALVALDVKPVGIA----DDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEI 116
                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                      65 EYSFVDALVALDVKPVGIADDNKKNRIIKPL-RDKIGKYTSVGTRKQPNLEEISKLKPDL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDG--DYNENIDAFKTISKALGKEEEG 174
                                                                                                                                                                                                                                                                                                                                                                                                                              KKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSN---SYVGQFLSQLGFKEA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 IKLLLVITLIIVFFKGCHSFLTQNIYSSNEYVKSTECRI-IKHKLGEICIPLNPQRIIVT 68
                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                   MRNSKPLLFLLTIVVVLAIAACNHN-----IPQSAKSQIATRTVSNTLGEVKVPLKPQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LKILSVIGLLFVLIA---TAACGNNSSSNSSKESSKDGVEIXHEEGTIKVPKHPKRVVVL
                                                                                                                                                                                              5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGV---EIKHEEGTTKVPKHPKRV
                                                                                                                                                                                                                                                                                                             56 VVLEENIVLDSVLALGIKPVGVAYCRECEEKFRGIPSDLLADVPVVGNIGT--QPSLEKI
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                                                                                                                      Length 319;
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                                                                                                                    ch 17.1%; Score 288.5; DB 2;
1 Similarity 29.9%; Pred. No. 2.5e-09;
93; Conservative 66; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKLNAVKNORV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 SKLKAVQNKQV 291
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Best Local S
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perior properties iron-compound-binding protein of iron(III) ABC transporter all0388 [imported C.Species: Nostco sp. PCC 7120
A;Note: Nostco sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                       C;Accession: ACL855
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shippo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: ACL855
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 < KUR>
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A;Experimental source: strain PCC 7120
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C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A89846
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 GIYKDINKIAPTIELKSFDGDYNEN-ID----AFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 YLKGPY--LQMNT---ETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 FVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 285; DB 2; Length 300; 26.0%; Pred. No. 3.6e-09; ive 64; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: al10388
C;Superfamily: ferrichrome-iron transport protein fhuD
                                       295 NHVYTVDSGYWIFGNILSANAILDDIVKYLVB 326
ORVDILDRDLWARSRGLISS --- EEMAKELVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Conservative
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iron([II]) dicitrate-binding periplasmic protein of ABC transporter alr2210 [imported] - C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AD2082
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Natanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Reference number: AB1807; MUID:21595285; PMID:11759840
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ferrichrome binding protein of ABC transporter all2147 [imported] - Nostoc sp. (strain F
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                                                                                                                               EQDIYPITSKIAPTVLLKFEHSGQWKE---VFTNTSVALGKTEVGQKVMENYYRRLAEFK 186
                                                                                                                                                                                                                                                                  187 QKMG-NKLSKIKVSV-----VRVYPDKINLYLLDSFCGTILQDAGLSRPESQNFTASEAT 240
                                                                                                                                                                                                                                                                                                                                                                                 241 ILFNNQIQMSISNELIEQADGDVIFIWTAENDAKGNQTAQYKLEQLKASPLWRNLKAVKE 300
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                                                                                       131 HKGIYKDLNKIAPTIELK-SFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYK
                                                                                                                                                                                                                   190 KEITMDKNOKVLPAVAAKSGLLAHPS-----NSYVGQFLSQLGFKEALSDDVTKGLSK
                                                                                                                                                                                                                                                                                                                                                243 YLKGPYLOM--NTETLSQVNPERMFIMT--NKASSNEPS---LKELEKDPVWKKLNAVKN
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16.5%; Score 279.5; DB 2;
Best Local Similarity 25.8%; Pred. No. 8.2e-09;
Matches 82; Conservative 75; Mismatches 130;
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C,Superfamily: ferrichrome-iron transport protein fecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 NKVYVVP-SYWIGS-GMLAANAIIDDL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 QRVDILDRDLWARSRGLISSEEMAKEL 322
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-330 <KUR>
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A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AD2134
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-31 kKIR.
A; Cross-references: UNIPROT:Q8YTT6; GB:BA000019; PIDN:BAB74326.1; PID:g17131720; GSPDB:G A; Experimental source: strain PCC 7120
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:
                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q99VN8; GB:BA000018; PID:g13700627; PIDN:BAB41924.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 ---TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAH-PSNSY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 VPKHPKRVVVLEYSFVDALVALDV-KPVGIADDNK---KNRIIKPLRD-----KIGKYTS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 VGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPS 277
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                                                               Stapylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 GGLVYDTLGF----NAVDKKVSNSNHGQ--NVSNEYVNKENPDVILAMDRGQAISGKST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 IGLLFVLIATAACGNNSSSNSSKESSKDGV-BIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
16.9%; Score 285; DB 2; Length 342
Best Local Similarity 28.9%; Pred. No. 4.2e-09;
Matches 101; Conservative 61; Mismatches 134; Indels
Lancet 357, 1225-1240, 2001
A,Title: Whole genome sequencing of meticillin-resistant
A,Reference number: A89758; MUID:21311952; PMID:11418146
A,Accession: A89846
A,Status: prelimary
A,Rolecule type: DNA
A,Residues: 1-342 <KUR>
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Best Local S:
Matches 92
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A; Residues: 1-357 < KUR>
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C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. Btrain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AD2085
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A; A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminarv
                                                                                                                      Rykazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001

SAFItie: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Recession: AE2074

A;Residues: Preliminary
A;Residues: 1-361 «KUR»
A;Genetics: Strain PCC 7120
C;Genetics: A;Genetics: A;Ge
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A;Molecule type: DNA
A;Residues: 1-319 <KUN>
A;Experimental source: strain PCC 7120
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C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2074
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDG--DYNENIDAFKTISKALGKEBEGKK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 LRLIQQNQKQRELTLSIEVLPKYDADILFIMTEHLTRDFKEANPEVLSFLQK-PIWSNLK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLEYSFV-DALVALDVKPVGI--ADDNKKNRIIKPLRDKIGKYTSVGT-RKQPNLEBISK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLN 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVE----IKHEEGTTKVPKHPKRVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.4%; Score 278; DB 2; Length 361; Best Local Similarity 29.3%; Pred. No. 1.1e-08; Matches 90; Conservative 63; Mismatches 124; Indels 30;
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C;Superfamily: ferrichrome-iron transport protein fecB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVKNORV 298
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AVKTKQI 333
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C;Species: Nostco sp. PCC 7120
A;Note: Nostco sp. prc 7120
A;Note: Nostco sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. DNA Res. 8, 205-213, 2001
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anc. A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8YUZ5; GB:BA000019; PIDN:BAB73885.1; PID:g17131277; GSPDB:CA;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iron(III) dicitrate-binding protein of ABC transporter alr2186 [imported] - Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 RKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGKBEBGKKRLEBHDKKIEBYKKBIT--MDKNQKVLPAVAAKSGL---LAHP-SNSYVGQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                      238
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---YLQMNTETLSQVNPERMFIMTNKASSNEPSLKEL----EKDPVWKKLNAVKNQRVDI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 PKRVVVLEYSFVDALVALDVKPVGIAD------DNKKNRIIKPLRDKI-GKYTSVGT 107
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                                                                                                                                                                                                                               134 IYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEBYKKEIT 193
                                                                                                                                                                                                                                                                --EPSLKELE----KDPVWKKLNAVKNORVDILDRDLWARSRGLISSE----EMAKELV 323
                                                                                                           ALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHKG 133
                                222 FLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSN-----
                                                                                                                                                                                                                                                                                                                                                                           5 VRGLKILSVIGLLFVLIATA----ACGNNSSSNSSKESSKDGVE---IKHEEGTTKVPKH
                                                                                                                                                                                                                                                                                                                                             194 MDKNQKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGLS-----KYLKGP
LFVLIATAACGNNSSSNSSKESSKDGVE---IKHEEGTTKVPKHPKRVVVLEYSFVDALV
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16.4%; Score 277.5; DB 2;
Best Local Similarity 27.3%; Pred. No. 1.2e-08;
Matches 98; Conservative 76; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | : : : | : | VDSSYWIFG-SILSANAIVDDLFKYLK 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LDRDLWARSRGLISSEEMAKELVELSK 327
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Nyferinate manes: reprincing process into the conference manes: reprincing process in the congression state and the congression states of costs.

Cipecession: Sa2930; C69622

Rischnesder, R.; Hantke, K.

Mol. Microbiol. 8, 111-121, 1993

A;Title: Iron-hydroxamate uptake systems in Bacillus subtilis: identification of a lipop A;Reference number: S32930; MuID:9326086; PMID:8388528

A;Accession: S32930; MuID:93260086; PMID:8388528

A;Accession: S32930; MuID:93260086; PMID:8388528

A;Rederence number: S32930; MuID:93260086; PMID:8388528

A;Rederence number: S32930; MuID:93260086; PMID:8388528

A;Residnes: 1-315 <SCH-
A;Residnes: 1-315 <SCH-
A;Residnes: 1-315 <SCH-
A;Residnes: 1-315 <SCH-
A;Residnes: C.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A; Enflich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Perrari, E.
A;Kunst, F.; Ogaswara, N.; Moszer, I.; Albertini, M.; Ruita, K.; Lapidus, A.; Galler; Icch, J.; Harwood, C.R.; Hematt, A.; Hilbert, H.; Holsappel, S.; Hospidus, A.; Galler; Icch, J.; Harwood, C.R.; Hematt, A.; Hilbert, H.; Holsappel, S.; Hospidus, A.; Harlo, K.; A; Harwood, C.R.; Harmatt, A.; Hilbert, M.; Kurita, K.; Lapidus, A.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucelly, M.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Harod, V.; Patr, M.; Patro, V.; Pohl, T.M.; Potrtelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Roche, M.; Sadate, Y.; Sato, T.; Sekowska, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, A.; Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; P.; Zumstein, B.; Yoshikawa, H.; P.; Danchin, A; Huthors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Panaka, T.; Panaka, T.
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 EITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLG-----FKEALSDDVTKGLSKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 LLLIAALAACGNNSESKGSASDSK-GAETFTYKAENGNVKIPKHPKRVVVMADGYYGYPK
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C,Superfamily: Bacillus subtilis ferrichrome ABC transporter fhuD
C,Superfamily: signal sequence #status predicted <SIG>
F,1-23/Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 315;
                                                                            - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 275; DB 2; Length 31
Pred. No. 1.4e-08;
2; Mismatches 121; Indels
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                                                                                     ferrichrome ABC transporter fhuD precursor - Bacillu
N;Alternate names: ferrichrome-binding protein fhuD
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32.1%;
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Best Local Similarity 32.1%
Matches 97; Conservative
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MD 290
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294 YFEPQMQKLKQQWSENAIAQSLTASKEGRVYFIPAYLCLGLPGPIGTELYLQELQKQLL 352
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288 VNSVDPLAQGGTAWSKVRFLKAAAE 312
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R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Edna Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An. A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AB2130

A;Status: preliminary

A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q8YTX0; GB:BA000019; PIDN:BAB74292.1; PID:g17131686; GSPDB:C
A;Experimental source: strain PCC 7120
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2130
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                                                                                                                                                                                                                                                                                                                                       240 EKQNQIPTSPGF-----PFVFASLERLDLLDADVMFVTLD--AGGEENFKKFQASPLMQ 291
                                                                                                                                                                                                                      ALGKEEBGKKRLEEHDKKIEEYKKEIT--MDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGFK-EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEK 283
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64
                                                  8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVE----IKHEEGTTKVPKHPKRVVV
-VEIKHEEGTTKVPKHPKRVVVL
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16.2%; Score 273; DB 2; Length 333;
Best Local Similarity 28.3%; Pred. No. 1.9e-08;
Matches 90; Conservative 65; Mismatches 127; Indels
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    14 IGLLFVLIATAACGNNSSSNSSKESSKDG-
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A;Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Recference number: AB1807; MUD:21595285; PMID:11759840
A;Recference number: AB1807; MUD:21595285; PMID:11759840
A;Residue: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-33 < kUN:A
A;Residues: 1-33 < kUN:A
A;Genetics: 1-33 < kUN:A
A;Genetics: Complete Co
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C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T36412
R; Saudited to the EMBL Data Library, September 1999
A; Reference number: 221606
A; Accession: T36412
A; Reference number: T36412
A; Restues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-350 cSAU>
A; Experimental source: strain A3(2)
                                        iron(III) dicitrate-binding periplasmic protein of ABC transporter all2157 [imported] C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GILHDIGILNPIFAE------SGDYDLPLSEELLPNIDSDILFIAPLR-KDDYSVIK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 PLKPQRIVTLDFNSFAALLALDTKPIATWITTBIEDDFPYFQGKAEGVEILRSSSG---- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 QFLSQLGFKEALSDDVTKGLSKYLKGPY-LQMNTETLSQVNPERMFIMTNKASSNEPSLK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKHPKRVVVLEYSFVDALVALDVKPVG-----IADD----NKKNRIIKPLRDKIGKYTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 VGTRKQPNLEEISKLKPDLIIA-DNNRHKGIYKDLNKIAPTIELKSFD--GDYNENIDAF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable iron-siderophore binding lipoprotein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RGLKILS----VIGLLFVLIATAACGNNSS-----SNSSKESSKDGVEIKHEEGTTKV
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16.2%; Score 274; DB 2; Length 343;
Best Local Similarity 26.5%; Pred. No. 1.8e-08;
Matches 91; Conservative 80; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 KLQQKPLWSKLKAVQQNQVYIVDFSVW-RGLNMLAAYAMLDDL 335
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C, Genetics:
C, Genetics:
C, Genetics:
C, Superfamily: iron(III) dicitrate transport protein
C, Superfamily: iron(III) dicitrate transport protein
16.2%; Score 274; DB 2;
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ferrichrome binding protein homolog lmo1959 [imported] - Listeria monocytogenes (strain Forecies: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG1319
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud; E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schlutetr, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Ritle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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                                                                                                                                                                                                                                                                                                                          69 VDALVALDVKPVG-----IADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISK 118
                                                                                                                                                                                                                                                                                                                                                                             : | | | : | : | - - - - - - DLGAPKF-NMEKLIA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 QNPDLIITVD----AKLLNREDEKAS 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 IIADNNRHKGIYKDLNKIAPTIEL-----KSFDGDYNENIDAFKTISKALGKEEEGKKRL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEHDKKIEEYKKEIT--MDKNQKV-LPAVAAKSGLLAHPSNSYVGQFL---SQLGFKEAL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GOFLSQ-LG
                                                                                                                                                                         9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
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C;Superfamily: Bacillus subtilis ferrichrome ABC transporter fhuD
                   Length 313;
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; Pred. No. 5.4e-08;
68; Mismatches 114; Indels
               ; Score 265; DB 2; Length 31; Pred. No. Se-08; 53; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 RLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYV--
                                                                                                                                                                                                                                                                                                                                                                                                         -DEVASLGANVVGTDSWAFPNTFLSKDQKKNMV--
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C,Genetics:
               15.7%;
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1 Similarity 26.0%;
82; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 WKKLNAVKNQRVDILDRD
                       Query Match
Best Local Similarity 29.2*
Matches 93; Conservative
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A;Molecule type: DNA
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                                                                                                                                                                         iron(III) dicitrate-binding periplasmic protein [imported] - Nostoc sp. (strain PCC 7120 (Species: Nostoc sp. Strain PCC 7120 (Species: 14-Dec-2001 #text_change 09-Jul-2004 (Spacession: A11943 (Spacession: A11944 (Spacession: A11943 (Spacession: A11944 (Spacession: A11943 (Spacession: A11943 (Spacession: A11943 (Spacession: A11944 (Sp
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A,Experimental source: strain PCC 7120
A;Genterial:
A,Gene: all:100
C;Superfamily: ferrichrome-iron transport protein fecB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LLFVLIATAAC----GNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDA
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KLKAVKNNCVYTVDSGYW
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Campylobacter jejuni

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enterochelin uptake periplasmic binding protein Cj1355 [imported]
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ABC transporter (binding protein) homolog yxeB - Bacillus subtilis

C;Species: Bacillus subtilis

R;Kungt, R; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter

C; Bron, S; Brouiller, S; Bruschi, C;V.; Caldwell, B; Capuano, V; Carter, N.M.; Char

A; Britich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Febret, C; Ferrari, E.

A;Authors: Poulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galler

Koetter, P; Koningsterin, G; Krodph, S; Kumano, M; Kuriet, K; Lapidus, A; Lardinois, A;Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A; Liu, H; Masuda, S; Mausel

Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H.; Parro, V; Pohl, T.M.; Portetelle

Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Scato, T; Scanlon, A;Authors: Schleich, S; Schroeter, H; Yanano, K; Yasumoto, K; Yata, K; Yoshida, K

A;Authors: Yoshikawa, H.F; Zumstein, E; Yoshikawa, H; Danchin, A; Tosato, V; Uchlyama,

T; Winters: P; Wipet, A; Yamamoto, H; Yamanok, K; Yasumoto, K; Yata, K; Yoshida, K

A;Accession: D70074

A;Accession: D70074

A;Accession: D70074

A;Experimental source: strain 168

C;Superfamily: Bacillus subtilis ferrichrome ABC transporter fhub
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                                                     220 QKDVLDGQD------WQKISLEVLPEFAADRMFVTTTSSGNAKDGEFTLKDLTNSPIWKD 273
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RESULT 33 H81279

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Cispecies: Campylobacter jejuni
Cispecies: Campylobacter jejuni
Cispecies: Campylobacter jejuni
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipates sion: HB1279
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir
R;Parkhill, J.; Wren, B.W.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf.
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues 1.330 cPAR.
A,Gross-references: UNIPROT:O9PMU4; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB7376
A,Experimental source: serotype O2, strain NCTC 11168
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
A;Variety: PCC 6803
C;Bace: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S74441
B;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N., O, X.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti:
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A;Cross-references: UNIPROT:P72593; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA165:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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73 VVILDLGILDTFDALKINDKVVGVPAKNLP-KYLQQFKNK----PSVGGVQQVDFEAINA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDV---TKGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVVLEYSFVDALVALDV - - KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISK
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A;Status: nucleic acid sequence not shown; translation not shown
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15.4%; Score 261; DB 2; Length 33
Best Local Similarity 26.3%; Pred. No. 9e-08;
Matches 88; Conservative 72; Mismatches 123; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 TKAAQNKKIIYLDPEYWYLASGNGLESLKTMILEI 325
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C;Superfamily: iron(III) dicitrate transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Keywords: iron transport
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hypothetical protein ABC-SBP [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F97988
C;Accession: F97988
C;Accession: FP, is Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. C, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; My, P.; Sun, P. M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Hitle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: F97988
A;Status: preliminary
A;Alatus: Apreliminary
A;Alatus: Apreliminary
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A;Cross-references: UNIPROT:Q97R09; UNIPROT:Q8DPY6; GB:AE007317; PIDN:AAK99738.1; PID:g1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DALVALDVKPVGIADDN---KKNRIIKP----LRDKIGKYTSVGTRKQPNLEEISKLKP
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                                                                              284 ALQKDPLLGKINAIKNGAVAVI 305
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Best Local Similarity 28.9%
Matches 93; Conservative
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C; Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: B5519
R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Reference number: A55000; MUID:21357209; PMID:11463916
A; Reference number: A55000; MUID:21357209; PMID:11463916
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-341 *KUR.
A; Residues: 1-341 *KUR.
A; Experimental source: strain TIGR4
C; Ganetics:
A; Ganetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                          146 ELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 FSETIGESWODNL----RLYGQALDREAEAEQLINDWDTRVAOMROKLSA-KDLTISLVRF 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 YFIYIGDSGDQTPGSITNPWLNHPLWQQLEVVQSGKAYAVSDVVWTTAGGIQAAHLLLDD 308
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                                                                                                                                                                 28 GETIQSNLTQRT-----IAHAMGVTAVPNEPQRIVVLTNEATDMVLALGVTPVGAVKSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 AKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -FIMTNKASSNEPS--LKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKE
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                                       Gaps
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28.9%; Pred. No. 2.3e-07;
ive 58; Mismatches 115; Indels
                                           Indels
   Pred. No. 9.6e-08;
64; Mismatches 136;
25.6%;
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Best Local Similarity 28.9°
Matches 93; Conservative
                                       77; Conservative
   Similarity
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   Best Local
Matches 7
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hypothetical protein BH1028 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C; Accession: D837AB R; Akasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir-Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-321 «KUR»
A;Gross-references: UNIPROT:Q8DNJ2; GB:AE007317; PIDN:AAL00490.1; PID:g15459362; GSPDB:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQ-LGFK--EALSDDV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 VATKNESSDKKALAILLNEGKMAAFGAKSRF-----SFLYQTLKFKPTDTKFEDS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWK 288
                                                                                                                   TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKA-----SSNEPSLKE--LEKDPVWK 288
128 OKFVDK-FKEIAPTVLFQASKDDYWTSTKANIESLASAFGETGTOKAKEELTKLDKSIOE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 RHG------QEVSFESVKEINPDILFVINRTLAIGGDNSSNDGVLENALIAETP---
                                                                                                                                       20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 KPVGIADDNKKNRIIKP-----LRDKIGKYTSVGTRKOPNLEBISKLKPDLIIADNNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 HKGIYKDLNKIAPTIELKSFDGDYNENIDA-FKTISKALGK--EBEGKKRLEEHDKKIEE
                                                               187 VATKNESSDKKALAILINBGKMAAFGAKSRF-----SFLYQTLKFKPTDTKFEDS
                                       --KKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQ-LGFK--EALSDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      hypothetical protein fatB [imported] - Streptococcus pneumoniae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 253; DB 2; Length 32
26.8%; Pred. No. 2.4e-07;
ive 66; Mismatches 117; Indels
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                                                                                                                                                                                                 289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                       Conservative
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A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Streptococcus pneumoniae
Cispecies: Old Hasquence_revision 03-Aug-2001 #text_change 09-Jul-2004
Cispecies on 3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
Cispecies on 3-Aug-2001
Rifected Spanner, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Helicapple, On, J.D.; Unmayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, On, J.J.; Lowis: Loftus, B.J.; Yang, Y. Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Reference number: A95000; MulD:21357209; PMID:11463916
A;Accession: G95218
A;Accession: G95218
A;Accession: G95218
A;Residues: L-321 ekURA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SP1872 [imported] - Streptococcus pneumoniae (strain TIGR4)
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                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                 | ::||:
234 LEKIGFQPVFLPDIERKPGLRP-----QITLETLAQLDADIVIVNTWVDNWNGKSTYT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSLKELE----KDPVWKKLNAVKNQRVDILDRDLWARSRGL-ISSEEMAKELVELSKKDS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPLKELKQKWAKNPILHNSQAWKEGRVYFVDYTLWGNVIGAPIANALILEQLPSLLLSNT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 LIATAACGNNSSSNSSKESSKDGVE--IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KILSVIGLLFVLIATAACGNNSSSNSSKES----SKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                        PNLEEISKLKPDLIIADNNRHKGIYKD---LNKIAPTIELKSFDGDYNENIDAFKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                      LGKEEEGKKRLEEHDKKIEEYKKEI--TMDKNQKVLPAVAAKSGLLAHPSNSYVG---QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                           Gaps
                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSQLGFKEALSDDVTK--GLSKYLKGPYLQMNTETLSQVNPERMFIMT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 321;
                                                                                    Length 349;
                                                                                  15.0%; Score 254; DB 2; Length 34 26.5%; Pred. No. 2.4e-07; ive 73; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.0%; Score 253; DB 2; 26.8%; Pred. No. 2.4e-07;
          Btrain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Conservative
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                        Similarity
96; Conserv
      A, Experimental source:
C, Genetics:
A, Gene: alr 2597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KK 332
                                                                                    Query Match
Best Local Si
Matches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: SP1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
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A,Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132
A,Accession: D83778
A,Accession: D83778
A,Residues: DNA
A,Residues: 1-329 <STO>
A,Cross-references: UNIPROT:09KE30; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A,Experimental source: strain C-125
C,Genetics:
A,Gene: BH1028
                                                                                                                                                                                                                                                                                                                                                              53 KVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 LEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNEN-IDAFK----TISKA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 FETIYDLQPDLIII-SGRTSEAYDELSDIAPTL---FVGLDTENYLESFRSNMETLGEI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 LGKBEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 FKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 V----TPVDENIEVSNHGQ--SISFEYIVEKNPDHLFVIDRGAVVQEGEETNIENELV- 288
                                                                                                                                                                                                                                                                                                               10 ILSVIGLLFVLIATAACGNNSSSN----SSKESSKDGVE-----IKHEEGTT 52
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                            Query Match
Best Local Similarity 25.6%; Pred. No. 3.5e-07;
Matches 86; Conservative 71; Mismatches 134; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 KKLNAVKNQRVDILDRDLWARS-RGLISSEEMAKEL 322
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Search completed: August 25, 2005, 09:27:10 Job time : 24 secs



GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

August 25, 2005, 09:27:00 ; Search time 163 Seconds Run on:

(without alignments)
807.548 Million cell updates/sec

US-10-724-972A-6352 1690

1 GVESVRGLKILSVIGLLFVL......EEMAKELVELSKKDSKKDNK 335 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1767149 segs, 392926209 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:\* Database :

| cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:\*
| cgn2 6/ptodata/2/pubpaa/BCO NEW PUB.pep:\*
| cgn2 6/ptodata/2/pubpaa/BCO NEW PUB.pep:\*
| cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:\*
| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:\*
| cgn2 6/ptodata/2/pubpaa/USO8 PUBCOMB.pep:\*

6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
6/ptodata/2/pubpaa/US10B\_NEW\_PUB.pep:\*
6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

ptodata/2/pubpaa/US10 NEW PUB.pep ptodata/2/pubpaa/US10E\_PUBCOMB. 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. prodata/2/pubpaa/US11A\_PUECOMB.pep: /prodata/2/pubpaa/US11\_NEW\_PUB.pep:\* /prodata/2/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_NEw\_PUB.pep: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:

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Result No.	Score	Query Match	Query Match Length DB ID	DB	ID	Description	
	1690	100.0	! ! !	18	US-10-724-972A-6352	Seguence	6352, Ap
7	1668		331	15	15 US-10-282-122A-71138	Sequence 71138, A	71138, A
e	1242			σ	US-09-815-242-12254	Sequence 1:	2254, A
4	1232	72.9	327	15	US-10-282-122A-43828	Sequence 43828, A	43828, A
'n	1181	6.69		0	US-09-815-242-5459	Seguence 5.	459, Ap
v	726	43.0	319	σ	US-09-815-242-5249	Sequence 5249, Ap	249, Ap
7	726	43.0		6	US-09-815-242-12122	Seguence 1.	2122, A
80	724.5	42.9		15	US-10-282-122A-41133	Sequence 44133, A	44133, A
σ	724.5		319	5	US-10-470-048B-329	Sequence	329, App
10	644			15	US-10-282-122A-71291	Sequence	71291, A
11	516.5			7	US-10-282-122A-66890	Segmence	66890, A

77. A	59, A	305, A	420, A	3, Ap	, Appl	93, Ap	6, App	, Appl	599, A	5, Ap	267, A	283, A	385, A	193, A	81, Ap	785, A	Appl	, Appl	, Appl	05, A	179, A	0, Appl	, Appl	, Appl	3, Ap	2, App	311, A	3, App	, Appl	46, Ap	54, A	Appli	84, Ap
Sequence 56054	Sequence 10469	Sequence 56	Sednence 69	Sequence 5193, Ap	Sequence 16	Sequence 51	Sequence 34	Sequence 16	Sequence 45599, A	Sequence 3875,	Sequence 53	Sequence 46	Sequence 45385, A	Sequence 46	Sequence 71	Sequence 68	Sequence 38,	Sequence 38	Sequence 38	Sequence 109	Sequence 46	Sequence 40,	Sequence 40	Sequence 40	Seguence 4403, Ap	Sequence 57	Sequence 47	Sequence 663, App	Sequence 12	Sequence 2046, Ap	Sequence 134	Sequence 9, Appli	Sequence 38
US-10-282-122A-56054	US-09-815-242-10469	US-10-282-122A-56805	US-10-282-122A-69420	US-08-781-986A-5193	US-10-278-946-16	US-10-329-624-5193	US-10-470-048B-346	US-10-967-189-16	5 US-10-282-122A-45599	US-09-738-626-3875	US-10-282-122A-53267	US-10-282-122A-46283	US-10-282-122A-45385	US-10-282-122A-46193	US-10-724-972A-7181	US-10-282-122A-68785	US-09-071-035-38	US-10-206-576-38	US-10-912-362-38	US-09-815-242-10905	US-10-282-122A-46179	US-09-071-035-40	US-10-206-576-40	US-10-912-362-40	US-09-738-626-4403			US-10-474-776-663			US-09-815-242-13454	US-10-415-478A-9	US-10-472-928-3884
12	σ	15	15	œ	14	15	17	17	15	6	15	15	15	15	18	15	σ	14	11	σ	15	σ	14	17	σ	15	15	16	16	17	σ	16	17
300	302	302	297	330	330	330	330	330	324	315	321	314	314	264	351	342	317	317	317	317	315	296	296	296	306	306	342	341	341	341	321	321	321
27.2	27.2	27.2	26.9	24.0	24.0	24.0	24.0	24.0	23.1	19.6	19.3	18.5	17.8									15.9	15.9	15.9	15.7	15.7	15.2	15.0	15.0	15.0	15.0	15.0	15.0
460	460	460	454	405	405	405	405	405	391	331	327	313	301	300	296.5	296	283	283	283	279	274.5	268	268	268	266	266	257.5	254	254	254	253	253	253
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATH03-16 FILE KEFEKENCE: FAITHOSING
CURRENT PELICATION NUMBER: US/10/724,972A
CURRENT PILING DATE: 2003-12-01
PRIOR PELING DATE: 1909-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/064,964
PRIOR APPLICATION NUMBER: 60/065,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 6352 Sequence 6352, Application US/10724972A Publication No. US20040147734A1 GENERAL INFORMATION: APPLICANT: Doucette-Stamm, Lynn APPLICANT: Bush, David TYPE: PRT; ORGANISM: S.epidermidis US-10-724-972A-6352 US-10-724-972A-6352

Gaps ö Length 335; 0; Indels 100.0%; Score 1690; DB 18, 100.0%; Pred. No. 6.8e-107; ive 0; Mismatches 0; Query Match 100. Best Local Similarity 100. Matches 335; Conservative

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181 IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 EYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV 63
                                                                                                                                                               MRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHBEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                         125 IADNNRHKGIYKDIAKIAPTIELKSFDGDYNBNIDAFKTISKALGKEEGKKRLEEHDKK
                                                                                                                                                                                                                                                                                                       KGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD
                                                                                                                5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DATE: A PAPLICANT: APPLICANT: APP
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   99.7%; Pred. No. 2.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 LWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 LWARSRGLISSEEMAKELVELSKKDSKKDNK 331
                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12254, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Staphylococcus aureus
US-09-815-242-12254
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Best Local Similarity 72.0%
Matches 236; Conservative
Best Local Similarity 99.7
Matches 330; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
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                                                                                         61 VVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                                                                                                                          PDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEB 180
                                                                                                                                                                                                                                                                                                                                                                                                                181 HDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGL 240
                                              VVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                          HDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - See File Wrapper or PALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLING DATE: 2000-03-21

PRIOR FLING DATE: 2000-05-23

PRIOR FLING DATE: 2000-05-26

PRIOR FLING DATE: 2000-05-26

PRIOR FLING DATE: 2000-05-26

PRIOR FLING DATE: 2000-09-06

PRIOR FLING DATE: 2000-09-06

PRIOR FLING DATE: 2000-09-09

PRIOR FLING DATE: 2000-10-27

PRIOR FLING DATE: 2001-02-27

PRIOR FLING DATE: 2001-02-07

PRIOR FLING DATE: 2001-02-07

PRIOR FLING DATE: 2001-02-07

PRIOR FLING DATE: 2011-02-07

PRIOR FLING DATE: 2011-02-07

PRIOR PLING DATE: 2011-02-07

PRIOR PRIOR
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US-10-282-122A-71138
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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Length 327;

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69.9%;
72.8%;
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APPLICANT: Haselbeck, Robert
                     Query Match
Best Local Similarity
Matches 235; Conserv
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                                                                                   184 KIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKY 243
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                                                                                                                                                                                                                                                                                                            LKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDR 303
                       69
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PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2010-01-09
PRIOR PILING DATE: 2010-01-09
PRIOR PILING DATE: 2010-01-09
PRIOR PILING DATE: 2010-02-16
TWRGLKTPSILGLIVALFLVAACGNTDNSSKKESSTKDTISVKDENGTVKVPKDAKRIVV
                                                                                                                                                                                                                                                    APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERDICE: ELITRA-034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                          304 DLWARSRGLISSEEMAKELVELSKKDSK 331
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Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Trawick, John
Carr, Grant
Yamamoto, Rober
Forsyth, R.
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US-10-282-122A-43828
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                                                                                                                                            5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
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APPLICANT: Chisen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
PRIOR APPLICATION NUMBER: US/09/815,242
CURRENT PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-10-23
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; Pred. No. 2.5e-72;
38; Mismatches 46;
72.9%; Score 1232; DB 15;
llarity 71.9%; Pred. No. 9.1e-76;
Conservative 42; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWARSRGLISSEEMAKELVELSKKDSK 331
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; ORGANISM: Staphylococcus aureus
US-09-815-242-5459
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Best Local Similarity 72.8<sup>†</sup>
Matches 225; Conservative
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59 YSFADYLAALDMKPVGIADDGSSKNITKSVRDKVGAYESVGSRPQPNMEVISKLKPDLII 118
                                                                                186 EEYKKEITWDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLK 245
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                                                                                                                                                                                              246 GPYLQMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKCINAVKNQRVDILDR 303
                                                                                                                                                                                                                    66 YSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLII
                                                                 ADNNRHKGI YKDLNKI APTI ELKS FDGDYNEN I DA FKTI SKALGKEEEGKKRLEEHDKKI
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47.1%; Pred. No. 2.2e-41;
tive 61; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Vimentiel Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SUGFWARE: FRALESEQ FOR WINDOWS VERSION 4.0
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity 47.1%
Matches 153; Conservative
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                                                                                                                                  KDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMD 195
                                                                                                                                                    196 KNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTET 255
                                                                                                                                                                                                                  LSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISS 315
                                                                                                                                                                                                                                                                                241 LADLNPERMIIMTDNAKKDSAEFKKLQEDPTWKKLNAVKNNRVDIVDRDVWARSRGLISS 300
                    6 RGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLE
   LLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVAL
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Best Local Similarity 47.1%; Pred. No. 2.2e-41;
Matches 153; Conservative 61; Mismatches 99,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5249, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // TYPE: PRT
// ORGANISM: Staphylococcus aureus
US-09-815-242-5249
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US-09-815-242-5249
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Sequence 329, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MELINE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
CURRENT APPLICATION UNMBER: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: PATENTING DATE: 2003-07-25
SOFTWARE: PATENTING DATE: 303
SOFTWARE: PATENTING SPECIFIC PATHOGEN
SEQ ID NO 329
LENGTH: 319
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                                                                                                               244 NEELANINPKYMILATDGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 KIKSELSKIAPTIMLVSGTGDYNANIEAFKTVAKAVGKEKEGEKRLEKHDKILABIRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 NEELANINPKVMILATDGKTDKNRTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VVFMLILVVAVAGGGGQKDT----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                                                                                                                                                                                     TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
                                                                               73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                      193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
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46.9%; Pred. No. 2.8e-41;
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300 GIIASESMAEDLEKIAEK 317
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300 GIIASESMAEDLEKIAEK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 GLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus aureus US-10-470-048B-329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 46.9
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             253
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT ELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200,488
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-24
                                                                  EBYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGLSKYLK 245
                                                                                                                                                                            GPYLOMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNORVDILDR
                                          ADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAPKTISKALGKEEEGKKRLEEHDKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15; Length 319;
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46.9%; Pred. No. 2.8e-41;
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                                                                                                                                                                                                                                                                                                                                                DLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                              Sequence 44133, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 46.99
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-282-122A-44133
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LENGTH: 319
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APPLICANT:
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13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL 72

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APPLICANT: Oyskind, Judith
APPLICANT: Oyskind, Judith
APPLICANT: Oxer, Grant
APPLICANT: Trawick, John
APPLICANT: You Hammoro, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITAA, 0.94A
CURRENT APPLICATION NUMBER: US/10/28, 122A
CURRENT APPLICATION NUMBER: US/10/19, 0.88
FRIOR APPLICATION NUMBER: 60/206, 948
FRIOR APPLICATION NUMBER: 60/206, 948
FRIOR PILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/230, 335
FRIOR PILING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: 60/230, 347
FRIOR PILING DATE: 2000-09-09
FRIOR APPLICATION NUMBER: 60/24, 578
FRIOR PILING DATE: 2000-12-2
FRIOR APPLICATION NUMBER: 60/25, 931
FRIOR PILING DATE: 2000-12-22
FRIOR PILING DATE: 2000-12-22
FRIOR PILING DATE: 2000-12-29
FRIOR PILING DATE: 2000-12-29
FRIOR PILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-08
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VVALEFSFVDALAALAVKFVGVADDNKPNRIIKPLKEKIGDYKSVGARKQPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VRGLKILSVIGLLFVLIATAACGNNSSSNS----SKESSKDGVEIKHEEGTTKVPKHPKR
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38.1%; Score 644; DB 15; Length 175;
Best Local Similarity 70.9%; Pred. No. 4e-36;
Matches 124; Conservative 23; Mismatches 24; Indels
Sequence 71291, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , окдаNISM: Staphylococcus haemolyticus
US-10-282-122A-71291
                                                                                                    APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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US-10-282-122A-66890

9 Sequence 66890, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

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APPLICANT: Vanamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-09-09
PRIOR PRILING DATE: 2000-10-23
PRIOR PRILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 TSVGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 TISKALGKEBEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 KIGDLIGKSKEMQARIAKHKQDIADIAK--TLPKGKKAIIGVSRETQFNLYNSESYAGGL 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 VEVLGYQMPKARADN-----QPNASVGLEQVAARKPDLMILIHYR---DESIARK 247
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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; Sequence 56054, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Pasteurella multocida
US-10-282-122A-66890
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                     Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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Best Local Similarity 38.1%
Matches 111; Conservative
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US20020061569A1

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                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION: IGENTIFICATION OF ESSENTIAL Genes in Microorganisms
FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-2-2
PRIOR PLING DATE: 2000-11-2-2
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-24
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-36
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PLING DATE: 2001-03-16
PRIOR PRIO
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Wang, Lianger

: Zamudio, Carlos

: Malone, Cheryl

:: Haselbeck, Robert

F: Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                           Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 35.8%
Matches 101; Conservative
                                                                                                                                                                                                  Wall, Daniel
Trawick, John
Carr, Grant
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US-09-815-242-10469 ; Sequence 10469, Application US/09815242

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45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
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                                                                                                                             APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Sammoto, Robert T.
APPLICANT: Xamamoto, Robert T.
APPLICANT: Will Howard
TITLE OF INVENTION: Identification of Essential Genes in FILIR OF INVENTION: Prokaryotes
FILIR DEFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Andlone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
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PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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US-09-815-242-10469
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US-10-282-122A-56805
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Best Local S
Matches 100
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APPLICANT:
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Query Match
Best Local S
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carric Carric
APPLICANT: Wamamoco, Robert
APPLICANT: Prevyth, R.
APPLICANT: PROPERTY ON HOUSER: BLITAN 034A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRILING DATE: 2000-05-36
PRIOR PRILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-09-09
PRIOR PLILING DATE: 2000-01-127
PRIOR PLILING DATE: 2000-01-127
PRIOR PLILING DATE: 2000-01-22
PRIOR PLILING DATE: 2001-02-09
PRIOR PLILING DAT
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PUDICation No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Applicantion Habelbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 100; Conserv
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US-10-282-122A-69420
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APPLICANT: TANACK, JOHN
APPLICANT: TANACK, JOHN
APPLICANT: Yamanoto, Robert
APPLICANT: Forent
APPLICANT: Forent
APPLICANT: Forent
APPLICANT: Forent
APPLICANT: Forent
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/200, 948
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/2030, 335
PRIOR APPLICATION NUMBER: 60/2030, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-01-22
PRIOR PILING DATE: 2000-01-22
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-01-02-16
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-05
PRIOR PILING DATE: 2001-03-05
PRIOR PILING DATE: 2001-03-05
PRIOR PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 PTEFVSLEQLLALDPNWLLVGHYRRPSIVDTWSKQPLWQVLGAVRNKQVAEVDGDSWARN 271
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US-08-781-986A-5193
; Sequence 5193, Application US/08781986A
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Ohlsen, Kari
Yaskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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RESULT 18
US-10-329-624-5193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
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Publication No. US20030054436A1
GENERAL INPORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
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; Pred. No. 1.5e-19;
65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENSON, BOD
REGISTRATION NUMBER: 90,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECHMONICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR EGO ID NO: 5193:
SEGUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-781-986A-5193
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32.8%;
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Best Local Similarity 32.8%
Matches 113; Conservative
                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
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Sequence 16, Application US/10278946 Publication No. US20030153733A1

RESULT 17 US-10-278-946-16

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Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOFLSQLGFKEALSDDVTKGL
APPLICANT: Simpson et al.

APPLICANT: Simpson et al.

TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides

FILE REFERENCE: P8461USD1

CURRENT APPLICATION NUMBER: US/10/278,946

CURRENT FILING DATE: 2002-10-24

PRIOR PRIING DATE: 2001-04-24

PRIOR PRIING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1998-03-20

PRIOR PRIING DATE: 1998-03-20

PRIOR PRIING DATE: 1998-04-01

PRIOR PRIING DATE: 1998-05-07

PRIOR PRIING DATE: 1998-05-07

SROID DATE: 1998-05-07

SROID DATE: P84-01

SROID DATE: P84-01

SROID DO 16

SROID NOS: 22

SROID NOS: 22

SROID NOS: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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Best Local Similarity 32.8%; Pred. No. 1.5e-19;
Matches 113; Conservative 65; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEB: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5193, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gil H. Choi
Patrick S. Dillon
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ORGANISM: Staphylococcus aureus
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SOFTWARE: Patentin version 3.1
SEQ ID NO 346
LENGTH: 330
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                                                                                                  US-10-470-048B-346
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                                                           TYPE: PRT
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Publication No. US20050037444A1
GRERAL INFORMATION:
APPLICANT: MEINKE BT AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATION AND PRODUCTION OF
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REPERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT APPLICATION NUMBER: US/10/470,048B
NUMBER OF SEQ ID NOS: 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 QKQVDNGKDIIQLTSKESIPLMNADHIPVVKSDPNAKDAALVKKTESEWTSSKEWKNLDA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INML-VVTLAFLLV-LAGCSGNSNKQSSDNKDKETTSIKHAMGTTEIKGKPKRVVTLYGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOPLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                MEDIUM TYPE: Diskete, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 466/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/329,624 FILING DATE: 27-Dec-2002 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171 FILING DATE: October 20, 1997 APPLICATION NUMBER: 60/009,861 FILING DATE: January 5, 1996 APPLICATION NUMBER: 08/781,966 FILING DATE: January 3, 1997 APPLICATION NUMBER: 108/781,966 FILING DATE: January 3, 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.0%; Score 405; DB 15; Length 330; 32.8%; Pred. No. 1.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Mismatches 132;
                                                                                                                                                                                                                                                                                                             NAME: MAIK J. Hyman
REGISTRATION NUMBER: 46, 789
REFERENCE/DOCKET NUMBER: PB248PID1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TYPE: procedin
MOLECULE TYPE: procedin
SEQUENCE DESCRIPTION: SEQ ID NO: 5193:
                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5193:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 330 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.81
Matches 113; Conservative
    COMPUTER READABLE
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US-10-470-048B-346
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                                                                                                                                                                                            8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
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TITLE OF INVENTION: Staphylococcus aureus Genes and Polypeptides
FILE REPERENCE: P8461USD2
CURRENT APPLICATION NUMBER: US/10/967,189
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 10/278,946
PRIOR PILING DATE: 2002-10-24
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1999-03-18
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-05-07
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                                                                            Length 330;
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                                                                                                                                       Indels
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                                                                            Query Match 24.0%; Score 405; DB 17;
Best Local Similarity 32.8%; Pred. No. 1.5e-19;
Matches 113; Conservative 65; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-967-189-16
, Sequence 16, Application US/10967189
; Publication No. US200509531995A1
; GENERAL INFORMATION:
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus aureus
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Matches 113; Conservative
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Best Local Similarity 34.4%;
Matches 116; Conservative 5
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                                                     63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                        128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                               188 YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                     241 SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                68 FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.091A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                          289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
                                                                                                                                                                                                                                                                                                                                                     293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-12-29
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45599, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus anthracis
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US-10-282-122A-45599
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ORGANISM:
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APPLICANT:
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Length 324;

DB 15;

23.1%; Score 391;

Query Match

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72 LVALDVKPVGIADDNKKARIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRH 131
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                                                                                                                                                  65 EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKOPNLEEISKLK 120
                                                                                                                                                                               178 LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                 LADMDKAFADAKAKİEKADLKDKNIAMAQAFTAKNVPTFRILT--DNSLALQVTKKLĞ-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                           230 EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 VAPLLGVALLLSSCSSTSSDESIQPEVASTGYSVEHAMGTTEIPETPTRVVVIDSPHLDA
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                                                                                                        3 KILSI----PIVVPLFAVGCGOOKEEKKETKADNKNOAITIKHAEGETKLDKPAKKVVVL
                                                             9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKD----GVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                              POLIIADNNRHKGIYKDLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEBEGKKR
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                     40;
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28.6%; Pred. No. 1.6e-14;
ive 65; Mismatches 140; Indels
                  Indels
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Pred. No. 1.4e-18;
9; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN NUMBER: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3875, Application US/09738626
Publication No. US20020197605A1
                       59;
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; Conservative
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IKEDA, MASATO
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FILE REFREENCE: Xu, H.
FILE REFREENCE: LITTRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
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                                              192 ITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQM 251
                                                                                                                                                                                                                                                                                                252 NTETLSQVNPERMF--IMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARS 309
                                                                                                                                                                                                                                                                                                                                                      243 SSENFGQIDGDLIFYTIPGSPEATTYPKISEL-----WUDSPAVRQGRTYEFEDBTWWVG 297
KGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKE 191
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 53267
LENGTH: 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 321;
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llarity 30.9%; Pred. No. 3e-14;
Conservative 55; Mismatches 136; Indels
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APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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APPLICATION NUMBER: 60/267,636
ALING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/253,625
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Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Best Local Similarity
Matches 99; Conserv
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US-10-282-122A-5326
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE OF INVENTION: 146atification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 02/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-02-09
PRIOR FILING PADELCATION NUMBER: 60/269,308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 HGQ--NITFEYIAKQNPEVMFVIDRGIATGSDVKESSTAKSVLANDIIKSMDAYKNDNII 292
                                                                                    71 ALVALDVKP--VGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLERISKLKPDLIIADN 128
                                                                                                                                                                                                                                                                  129 NRHKGIYKDLNKIAPTIBLKSFDGDYNE----NIDAFKTISKALGKEBEGKKRLEBHDKK 184
67
                                                                                                                                             11 IAIIGLVTVF---ALGGSKKNESKTSENSNNTIKITHNLGETDVKLNPKKVVVFDYSALD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 YLDSPTWYVNDGGLTSLNKM 312
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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, ORGANISM: Bacillus anthracis
US-10-282-122A-46283
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-46193
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SEQ 1D NO 45385
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APPLICANT:
APPLICANT:
APPLICANT:
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/201,038
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING PILING DATE: 2001-02-09
PRIOR PILING PIL
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                                                                                                                                                                                                                                      9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF
                                                                                              32;
         DB 15; Length 314;
         18.5%; Score 313; DB 15; Length 3
29.9%; Pred. No. 2.6e-13;
ive 65; Mismatches 135; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Disen, Kari
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: 
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Yamamoto, Robert
    Query Match
Best Local Similarity 29.94
Matches 99; Conservative
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US-10-282-122A-45385
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APPLICANT:
APPLICANT:
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APPLICANT: FORSYth, R.
APPLICANT: Vu, H.
APPLICANT: Xu, H.
CURRENT ELITRA.034A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 LSDDV----TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 IFNDLKLPAVKGTP--TDKPLVQVQKEALIDYNPDYLFVFTTGDGSQR--LKEFQEESIW 272
                                                                                                                                                                                                                                                      16 LLFVLIAT----AACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVVLBYSFVD
                                                                                                    Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Mismatches 106;
                                                                                                          17.8%; Score 301; DB 15; 27.3%; Pred. No. 1.7e-12;
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
TYPE: PRT ORGANISM: Bacillus anthracis
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Yamamoto, Robert
Forsyth, R.
                                                                                                          Query Match
Best Local Similarity 27.3*
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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DKKKISNTVEVPKNPKNAVVLDYGALDVL----KELGVADKVKGLPKGENNQSLPKFLD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                              286 DRGSVVGGKATTN-----QVLKNKVIKNVKAVKSNHIYELDPKLMYFSGG--SSTTTIKQ 338
                                                                                                              155 NENI--DAFK---TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSG 209
                                                                                                                                                                                                                            321
                                                                               --KIGKYTSVGTRKQPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDY 154
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLADICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLICATION NUMBER: 60/230,347
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
                                                                                                                                                                                                                                                                                                                                                                                                         262 ERMFIMTUKASSNEPSLKELEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKE
                                                                                                                                                                                                                                                                                                   210 LLAH-PSNSYVGQFLSQLGPKEALSDDVTKGLSKYLKGPYLQ-MNTETLSQVNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 18/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 68785, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Halone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : ||::
339 IDELNE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVELSK 327
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SEQ ID NO 68785
LENGTH: 342
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APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH03-16
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT APPLICATION NUMBER: 09/450,969
PRIOR PILING DATE: 1990-11-29
PRIOR PILING DATE: 1990-08-13
PRIOR PILING DATE: 1990-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 EYSFVDALVALDVKPVGIADDNKKNRII-----KPLRDKIGKYTSVGTRKQPNLEEISKLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PDLIIADNNRHKGIYKDLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEHDKKIEBYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EWVYSEDLIALGVQPVGMADIKNYNKWVNTKTKPSKDVV----DVGTRQQPNLEEISRLK
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
  PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 46193
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVBIKHE--
                                                                                                                                                                                                                                                                                                                                     Length 264;
                                                                                                                                                                                                                                                                                                                               ; Score 300; DB 15; Length 26
; Pred. No. 1.6e-12;
50; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.5%; Score 296.5; DB 18; Length
Best Local Similarity 28.4%; Pred. No. 4e-12;
Matches 104; Conservative 70; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7181, Application US/10724972A; Publication No. US20040147734A1; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                            17.8%;
Local Similarity 33.6%;
les 93; Conservative 5
                                                                                                                                                                                                                                             , ORGANISM: Bacillus anthracis
US-10-282-122A-46193
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US-10-724-972A-7181
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US-10-724-972A-7181
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LENGTH: 351
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Best Local S
Matches 93
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Length 317;

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Query Match
16.7%; Score 283; DB 9; L
Best Local Similarity 30.4%; Pred. No. 2.9e-11;
Matches 101; Conservative 59; Mismatches 130;
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INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Sequence 38, Application US/10206576; Publication No. US20030017495A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 317 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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US-10-206-576-38
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Publication No. US20020045737A1
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                          EEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTK 238
                                                                                                                                                                                                                                                                                                                                        254 GSHGNI-----VNSELLLKINPDWMFVIDRDAAIGREDSQPA-KQVLDNALVRKVNAWN 306
                                                                                                                                                                                                                                               LIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAF----KTISKALGKEEGKKRL 178
                                                                                                                                                                                                                                                                                                                                                                                          GLSKYLKGPYLQMNTETLSQVNPERMFIMTNKAS----SNEPSLKELEKDPVWKKLNAVK 294
                                                                                                                         9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSF 68
                                                                                                                                                                     69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYT-----SVGTRKQPNLEBISKLKPD
                                                            34;
                          DB 15; Length 342;
                        17.5%; Score 296; DB 15; Length 3
29.2%; Pred. No. 4.2e-12;
ive 66; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Andere Brookes
REGISTRATION NUMBER: 36,373
REPERBONE/DOCKET WOMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 317 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                              90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-071-035-38
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COMPUTER READABLE FORM:
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                        Query Match
Best Local Similarity
Matches 90; Conserv
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GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polymucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
                                                                                                                                                       68 FVDALVALDY--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDLII 125
                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 KGLSKYLKGPYLQMNTETLSOVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 ADNNRHKGIYKDINKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                             122 I-SGRQQDYQBQLKAİAPTİYLAVDAKAPWASTKQNİETLGTİ---FDKEEVAKEKİTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                 178 EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST
                                                11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                              67 SLDTMDALGVGDRVVGAPTKN----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLII
                                                                                                                                                                                                                                                                                                                                                                                 182 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT
Gaps
42;
Indels
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APPLICATION NUMBER: US 09/071,035
FILING DATE: 1990-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 314
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKBEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 DKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELBKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                            11 VSMMGLIML---SACQTNKKTADSATTETTAKTEVTVKDTNGQLTVPKNPKKVVVFDNG
                                                                                                                                                                                                                                                                                                                                                                                                                               178 EKEIADVKKQAEASAN-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEAST
                                                                                                                                                                                                                                                                                           11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                              68 FVDALVALDV - - KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLÆEISKLKPDLII
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                           Indels 42;
                                                                                                                                                                                      Query Match
16.7%; Score 283; DB 17; Length 317;
Best Local Similarity 30.4%; Pred. No. 2.9e-11;
Matches 101; Conservative 59; Mismatches 130; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haselbeck, Rousel,
APPLICANT: Oblsen, Kari L.
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramacto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FILE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SOUTHARE: PRIOR PRICE PRACE
TYPE: PRT
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        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10905, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-815-242-10905
                                                                                                                                        US-10-912-362-38
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Publication No. US20050043528A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 14200 Shady Grove Road
                                                                                                                                                                                                                                                                                                 68 FVDALVALDV--KPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLII 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 I-SGRQQDYQEQLKAİAPTİYLAVDAKNPWASTKQNİETLGTİ---FDKEEVAKEKITGL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 KGLSKYLKGPYLOMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 HGQS------VSYEYVLEKNPGILFVVDRTKAIGGDDSKDNVAANELIQKTDAGKND 285
                                                                                                                                                                                                                                                                                                                                                 67 SLĎTMDÁLGVGDRVVGAPTKN----IPAYLKKYQKVESAĞGIKEPDLEKINQLKPDLII 121
                                                                                                                                                                                                                                                                                                                                                                                                    126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                              11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                           42;
                                                                                           Length 317;
                                                                                     16.7%; Score 283; DB 14; Length 3 30.4%; Pred. No. 2.9e-11; ive 59; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 RVDILDRDLWARSRGLISSEEMAKELVELSKK 328
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APPLICATION NUMBER: US 10/206,576
FILING DATE: 2002-07-29
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1999-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 KVIMLQPDVWYLSGGGLESMHL---MIEDVKK 314
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REGISTRATION NUMBER: 46,789
REPREBUCE/DOCKET NUMBER: PB369PID2
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/912,362
FILING DATE: 06-Aug-2004
PRIOR APPLICATION DATA:
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-206-576-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 2000
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 317 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
                                                                                                                Best Local Similarity 30.44
Matches 101, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                           Query Match
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STATE: Maryland
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US-09-071-035-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                             238 KGLSKYLKGPYLQMNTETLSQVNPERMFIM-TNKASSNEPSLKELEKDPVWKKLLNAVKNQ 296
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                                                                                                                                                                                                                            126 ADNNRHKGIYKDLNKIAPTIEL----KSFDGDYNENIDAPKTISKALGKEBEGKKRLEEH 181
                                                                                                                                                                      99
                                                                                                                                11 LSVIGLLFVLIATAACGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                          Gaps
                                                                                            42;
                                                          Length 317;
                                                    Query Match
16.5%; Score 279; DB 9; Length 31
Best Local Similarity 30.1%; Pred. No. 5.4e-11;
Matches 100; Conservative 60; Mismatches 130; Indels
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
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PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/203
PRIOR PLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-10-23
PRIOR PLILOTATION NUMBER: 60/253,625
PRIOR PLILOGATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
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FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
; ORGANISM: Enterococcus faecalis US-09-815-242-10905
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-46179
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APPLICANT:
APPLICANT:
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Sequence 40, Application US/09071035
Publication No. US20020045737A1
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          71 ALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 DKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGOFLSQLGFKEALSDDVTKGLS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 KYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLK----ELEKDPVWKKLNAVKNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 HKGIYKDLNKIAPTIE-----LKSFDG--DYNENIDAFKTISKALGKEEEGKKRLEEH 181
                                                                                                                                                                                                                                                                                                                                                       10 AILSIFFLLIGCSAKGDEKASATKTEKGKEKIEVTDLSGRKVTFDKVPESFATLSMGDMN
                                                                                                                                                                                                                                                                                                                          12 SVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEG-TTKVPKHPKRVVVLEYSFVD
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 46179 LENGTH: 315
                                                                                                                                                                                                                        Query Match
16.2%; Score 274.5; DB 15; Length 315;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 92; Conservative 70; Mismatches 129; Indels 45;
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 RVDILDRDLWARSRGLISSEEMAKELVELSKKDSKK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/071,035
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   ) ORGANISM: Bacillus anthracis
US-10-282-122A-46179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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us-10-724-972a-6352.rapb

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US-10-912-362-40
| Sequence 40, Application US/10912362
| Sequence 40, Application US/10912362
| Publication No. US20050043528A1
| Publication No. US20050043528A1
| GENERAL INFORMATION:
| APPLICANT: Choi et al.
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
| TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GAPTKN-----IPAYLKKYQKVESAGGIKEPDLEKINQLKPDLII-SGRQQDYQEQLKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 IAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 NQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VTKGLSKYLKGPYLQMN 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.9%; Score 268; DB 14; Length 296;
Best Local Similarity 30.3%; Pred. No. 2.8e-10;
Matches 96; Conservative 54; Mismatches 129; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                     Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/912,362
PILING DATE: 06-Aug-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 10/206,576
FILING DATE: 2002-07-29
APPLICATION NUMBER: US 09/071,035
FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
REFERENCE/DOCKET NUMBER: PB369P1D1
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40: 05-10-206-576-40
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COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows 2000
SOFTWARE: ASCII Text
                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 LISSEEMAKELVELSKK 328
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Publication No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 IAPTIEL----KSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMDK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 NOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDD----VTKGLSKYLKGPYLQMN 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CGNN---SSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDV--KPV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 N-NALVVLVNEGQLSAYGKGSRFGLIHDTFGFKAA--DDKIEASTHGQS-----VS
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                                                                                                                                                                                                                                                                            Length 296;
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1 Similarity 30.3%; Score 268; DB 9; Length 296
1 Similarity 30.3%; Pred. No. 2.8e-10;
96; Conservative 54; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/071,035

FILING DATE: 1998-05-04

APPLICATION NUMBER: US 60/046,655

FILING DATE: 1997-05-16

APPLICATION NUMBER: US 60/044,031

FILING DATE: 1997-05-06

APPLICATION NUMBER: US 60/066,009

FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
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OPERATIOS SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-U1-2002
CLASSIPICATION: 
    UNKNOWN>

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REGISTRATION NUMBER: 46,789
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   SEQUENCE CHARACTERISTICS:

JENGTH: 296 amino acide
TYPE: amino acid
STRANDEDNESS: single
JOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-40
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COMPUTER READABLE FORM:
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Best Local &
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Gaps

40;

DB 9; Length 306;

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Query Match
Best Local Similarity 25.9%; Pred. No. 4e-10;
Matches 82; Conservative 60; Mismatches 135; Indels
                   ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 572, Application US/10627476 Publication No. US20040030116A1
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                         ; ORGANISM: COLY;
US-09-738-626-4403
TYPE: PRT
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                                                                                                                                                                                                                                                                                                            Length 296;
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Best Local Similarity 30.3%; Pred. No. 2.8e-10;
Matches 96; Conservative 54; Mismatches 129; Indels
                                                                                  REPERENCE/DOCKET NUMBER: PB369P1D2
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-912-362-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4403, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
      FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
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LENGTH: 306
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73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK 132
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GENERAL INCRAMINED.

GENERAL INCRAMINED.

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Hartwig

APPLICANT: Schoder, Gregor

APPLICANT: Schoder, GRegor

TITLE OF INVENTION: CORTNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

TITLE OF INVENTION: TRANSPORT

TITLE OF INVENTION: TRANSPORT

TITLE OF INVENTION: TRANSPORT

TITLE OF INVENTION: TRANSPORT

TITLE OF INVENTION: TRANSPORT

TITLE OF INVENTION: TRANSPORT

CURRENT APPLICATION NUMBER: US/10/627,476

CURRENT FILING DATE: 1099-06-23

PRIOR FILING DATE: 1099-06-23

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR PELICATION NUMBER: DE 19931454.3

PRIOR PELICATION NUMBER: DE 19931459.3

PRIOR APPLICATION NUMBER: DE 19931212.1

PRIOR APPLICATION NUMBER: DE 19931212.1

PRIOR APPLICATION NUMBER: DE 19931212.1

PRIOR APPLICATION NUMBER: DE 19932122.1

PRIOR APPLICATION NUMBER: DE 19932122.6

PRIOR APPLICATION NUMBER: DE 19932125.6

PRIOR PELING DATE: 1999-07-09

PRIOR PELING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09

PRIOR PELING DATE: 1999-07-09

PRIOR PELING DATE: 1999-07-09

PRIOR PELING DATE: 1999-07-09

PRIOR PELING DATE: 1999-07-09

PRIOR PELICATION NUMBER: DE 19932128.0

PRIOR PELICATION NUMBER: DE 19932128.0

PRIOR PELICATION NUMBER: DE 19932128.0

PRIOR PELICATION NUMBER: DE 19932128.0

PRIOR PELING DATE: 1999-07-09

PRIOR PELICATION NUMBER: DE 19932128.0
                                             17 LFVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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SEQ ID NO 572
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 DVEGKTVNMIRPRDEQTMSLYGPTSFAGSSLECAG----
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TYPE: PRT
ORGANISM: Burkholderia cepacia
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US-10-282-122A-47311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 DDLQADIAPENFWLATADYVFVTATDVTDENELPEVIRE-----NREQFPSLTLVDTSY 281
                                                                                                                                                                                  11 LIVLLAAALPLTACSSSSEREASTSSATR--EPTDAHGTTEVPENPORVVULEPLELDTA 68
                                                                                                                                                           17 LFVLIATA----ACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                    Gaps
                                                                                                                    40;
                                                                             DB 15; Length 306;
                                                                           15.7%; Score 266; DB 15; Length 3
Larity 25.9%; Pred. No. 4e-10;
Conservative 60; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION INDMER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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i TYPE: PRT
i ORGANISM: Corynebacterium glutamicum
US-10-627-476-572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
APPLICATION NUMBER: 2001-02-09
APPLICATION NUMBER: 60/269,308
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
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Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
Trawick, John
                                                                           Query Match
Best Local Similarity
Matches 82; Conserv
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US-10-282-122A-47311
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Sequence 663, Application US/10474776
Publication No. US20040110181A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WHOCH
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 663
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 47311
LENGTH: 342
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; Pred. No. 3e-09;
58; Mismatches 115; Indels 56
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein August 25, 2005, 09:18:46; Search time 167 Seconds (without alignments) 775.837 Million cell updates/sec .. 0 Run

Perfect score:

US-10-724-972A-6352 1690 1 GVESVRGLKILSVIGLLFVL.....EEMAKELVELSKKDSKKDNK 335 Sequence:

BLOSUM62 . Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched: 2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

A\_Geneseq\_16Dec04:\* Database :

geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADIES

SUMMARIES	Description	7057 Ads07057 Staphyloc	3214 Abu43214 Protein e	661 Staphyloc	1865 Staphyloc	Abu15904	Abr38894	Abm73426					Abu16209	Abr38895	1867 Abr41867 Staphyloc		3367 Abu43367 Protein	Abu38966		Abu28130	4876 Aau34876 E. coli	Abu28881	1496 Abu41496 Protein	9745 Aaw89745 Staphyloc	2331 Aay42331 Staphyloc	A COLOR DE LA COLO
S	£	ADS07057	ABU43214	AAU36661	ABR41865	ABU15904	ABR38894	ABM73426	AAU33963	AAU33753	AAU36529	ABJ19052	ABU16209	ABR38895	ABR41867	ABM72855	ABU43367	ABU38966	ABM68354	ABU28130	AAU34876	ABU28881	ABU41496	AAW89745	AAY42331	
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d	Query Match	100.0	98.7	73.5	73.0	72.9	72.7	71.8	69.9	43.0	43.0	42.9	42.9	42.9	42.9	42.9	38.1	30.6	28.2	27.2	27.2	27.2	26.9	24.0	24.0	
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ABJ19069	ABR38893	ABR41864	ADF43556	ABU17675	ABG08851	ABG13148	ABM73050	AAG90121	ABU25343	ABU18359	ADC94889	ABU17461	ABU18269	ABP40647	ADS07886	ABU40861	ADF06577	AAG82087	AAG81684
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330	330	330	330	324	1132	932	287	315	321	314	352	314	264	351	351	342	351	347	347
24.0	24.0	24.0	24.0	23.1	22.2	20.7	20.3	19.6	19.3	18.5	18.2	17.8	17.8	17.5	17.5	17.5	17.5	17.3	17.3
405	405	405	405	391	375	350	343	331	327	313	307.5	301	300	296.5	296.5	296	296	292	292
26	27	28	6	0.6	31	32	33	3.4	35	36	37	38	36	4	41	42	43	44	45

## ALIGNMENTS

antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; Staphylococcus epidermis polypeptide seqid 6352. ADS07057 standard; protein; 335 AA Staphylococcus epidermidis. (first entry) computer based system. 04-NOV-2004 ADS07057; RESULT 1 ADS07057 

US2004147734-A1.

29-JUL-2004.

97US-0064964P. 98US-00134001. 99US-00450969. 01-DEC-2003; 2003US-00724972 08-NOV-1997; 13-AUG-1998; 29-NOV-1999;

(DOUC/) DOUCETTE-STAMM L. (BUSH/) BUSH D.

Bush D; Doucette-Stamm L,

WPI; 2004-580138/56. N-PSDB; ADS03285.

New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.

Claim 17; SEQ ID NO 6352; 741pp; English

The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 13772) and encoding an Staphylococus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector, a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a

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aubject for S. epidermidis infection; a recombinant or aurier; treating a nucleic acid cited above and a carrier; treating a pure preparation of an S. epidermidis polypoptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus nucleic acid in a sample; a computer readable medium having recorded in it the nucleotide system for identifying fragments of the Staphylococcus genome of system for identifying fragments of the Staphylococcus genome of the Staphylococcus genome of commercial importance; identifying an expression modulating fragment of commercial important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermids proterial confidencial in the amino acid sequence of a S. epidermids protein of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDKKI EBYKKEI TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDKKI EEYKKEI TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  composition for prevention or treatment of an S. epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1690; DB 8;
100.0%; Pred. No. 1.5e-129;
ive 0; Mismatches 0;
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
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Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 335 AA;
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                                                                                                                                                                                                                                                                                                                                                   the invention
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid cancilled and a promoter operably linked to the nucleic acid conclaining the vector; (3) an isolated conclaining the vector; (3) an isolated by the antisense antisense call containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits spilling a product is oversypressed or undersypressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a product is oversypressed or undersypressed; (12) determining the extent compound; a activity; (11) a culture comprising strains in which the test compound that inhibits and collection of pathway in which a proliferation required gene or its gene product lies conduct is oversypressed or undersypressed; (12) determining the extent conduct is oversypressed or undersypressed; (12) determining the extent conduct is oversypressed or undersypressed; (12) determining the compound of a collection of strains is proliferation of an organism. The antisense nucleic acids required for proliferation in cells other candidate molecic acids required for proliferation in cells other than S. aureus, S. typhimurlum, continued for proliferation in cells other promoted as encoded by one of the target prokaryotic essential genes requence is encoded by one of the target prokaryotic desential genes production, of the promoted of the p
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                                                                                                                                                                                                                                         screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYSPVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYSFVDALVALDVKPVGI ADDNKKNRI I KPLRDKI GKYTSVGTRKQPNLEBI SKLKPDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                                                       Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9.2e-128;
l; Mismatches 0;
                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                             25; SEQ ID NO 71138; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.7%;
Best Local Similarity 99.7%;
Matches 330; Conservative 1
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                              (ELIT-) ELITRA PHARM INC.
                                                                                                       Zamudio C,
Trawick JD,
                                                                                                                                                                        2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 331 AA;
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LKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDR

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123

LEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLKPDL

63 69

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10 TWRGLKTPSILGLIVALFLVAACGNTDNSSKKESSTKDTISVKDENGTVKVPKDAKRIVV
                                                                                                                                                          124 IIADNNRHKGIYKDLNKIAPTIELKSPDGDYNENIDAFKTISKALGKEEEGKKRLEEHDK
                                                                                                                                                                                                        184 KIEBYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKY
           4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
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ID ABR4
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241 KGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                                                                                         Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                             Staphylococcus aureus cellular proliferation protein #831.
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                              LWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                   LWARSRGLISSEEMAKELVELSKKDSKKONK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 12254; 511pp; English.
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                                                                                                                                               AAU36661 standard; protein; 337
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2000US-0206848P.
2000US-0207727P.
2000US-0253625P.
2000US-0253625P.
2000US-0257931P.
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                                                                                                                                                                                                               (first entry)
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Yamamoto RT, Xu HH;
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                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
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23-OCT-2000;
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22-DEC-2000;
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The present sequence is that of a novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP). To isolate SEIP genes, an expression library of S. aureus genomic DNA was screened with anti-SEIP antisera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The present SEIP has sequence homology with the siderophore family of periplasmic binding proteins. The invention provides methods be used indantification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococcal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                                                                                                                                                                                               Staphylococcal surface-exposed immunogenic polypeptide D2 SA03.
                                                                        DLWARSRGLISSEEMAKELVELSKKDSK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
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                                                                                                                                                                           ABR41865 standard; protein; 337 AA
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                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                        antibacterial; vaccine
                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
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Gaps

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Best Local Similarity 72.0% Matches 236; Conservative

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ABR38894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                70 LEYSFADALAALDVKPVGIADDGKKKIIKPVREKIGDYTSVGTRKQPNLEEISKLKPDL 129
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                                                                                                                                                                                                                               309
                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                             10 TMRGLKTFSILGLIVALLLVAACGNTDNSSKKESSTKDTISVKDENGTVKVPKDAKRIVV
                                                                                                                                                  4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
                                                                                                       LEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDL
                                                                                                                                         1 I ADNNRHKGI YKDLNKI APTI ELKSFDGDYNEN I DAFKTI SKALGKEEEGKKRLEEHDK
                                                                                                                                                                           KI EEYKKEI TMDKNQKVI.PAVAAKSGILAHPSNSYVGQFI.SQLGFKEALSDDVTKGLSKY
                                                                                                                                                                                                              LKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDR
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¥5
                                                    Gaps
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Xu HH;
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                                  Length 337;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #1431.
                                  DB 6;
                                 73.0%; Score 1233; DB 6;
larity 71.6%; Pred. No. 3.3e-92;
Conservative 43; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 43828; 1766pp; English
                                                                                                                                                                                                                                                           DLWARSRGLISSEEMAKELVELSKKDSK 331
                                                                                                                                                                                                                                                                                                            ABU15904 standard; protein; 327 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926/02.
N-PSDB; ACA19774.
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Trawick JD,
                                          Similarity
diagnostic assays
                  Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   WO200277183-A2
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                                   Query Match
                                            Best Local
Matches 23
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (5) inhibiting cellular to proliferation or the activity of a gene in an operon required for proliferation or that has an activity agency required for proliferation or that has an activity agency required for proliferation, (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or that that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity, (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity, (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for groliferation of an organism. The antisense nucleic acids are useful for for acellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence acids required for proliferation in cells other than S. aureus, S. typhimurium, C. patent did not form part of the printed sequence assential genes necessity from WIPO at the target prokaryotic essential genes where the sequence data for this continued for proliferation of an organism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVL
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Matches 235; Conservative
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20-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 TMRGLKTFSILGLIVALLLVAACGNTDNSSKKESSTKDTISVKDENGTVKYPKDAKRIVV 69
                                                                                                                                                                                                                Isolating microbial target surface exposed immunogenic polypeptides, by immunizing host with microbial membrane-associated polypeptides to produce antibodies and using antibodies to isolate target polypeptides.
                                                                                                                                                                                                                                                                              The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Pharmaceutical compositions based on the polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in a patient. They are also useful for topical disinfection in an animal or mammal e.g. human. The current sequence represents an SEIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 LINKYKDEIKFDRNOKVLPAVVAKAGLLAHPNYSYVGOFLNELGFKNALSDDVTKGLSKY
exposed immunogenic polypeptide; iron-binding; receptor; fungicide; protozoacide; infection; disinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SVRGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                   72.7%; Score 1228; DB 6; 71.3%; Pred. No. 8.4e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Mismatches
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                                                                                                                                                                                                                                                             Claim 15; Page 40-41; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM73426 standard; protein; 348 AA.
                                                                                                 10-JUL-2002; 2002WO-US021663
                                                                                                                         10-JUL-2001; 2001US-0304390P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                           WPI; 2003-221756/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 337 AA;
                                                       WO2003006672-A2
           antibacterial;
                                                                            23-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes and encoded proteins from sition comprising the S. aureus protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein, useful as a vaccine for treating or infection, specifically an infection caused
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                                                  Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5332; 49pp; English
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Staphylococcus aureus protein #2666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to novel
                                                                                                                                                                                                                                                                                                 27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001; 2001GB-0007661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preventing Staphylococc
S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mora M,
                                                                                                                                 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120786/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ACF74986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 348 AA;
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RESULT 8

ABM73426;

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antibodies capable of binding to the expressed proteins. The proteins can antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety
        KDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITMD 195
                                                                                            241 LADLNPERMIIMTDNAKKDSAEFKKLQEDPTWKKLNAVKNNRVDIVDRDVWARSRGLISS
                            256 LSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISS
                                                                         KNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus cellular proliferation protein #29.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 5249; 511pp; English.
                                                                                                                                                                                                                                                                                                                                AAU33753 standard; protein; 319 AA.
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2000US-0207727P.
2000US-0242578P.
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22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                              316 EEMAKELVE 324
                                                                                                                                                                                                                                              EEMAKELVE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus.
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Yamamoto RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prokaryotic cellular proliferation, their use in identifying the genes, prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli, staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, coli seful for the identification of potential new targets for antibiotic consection protein neucleic acids compounds in rational drug discovery programmes. The proteins antisense nucleic acid sequence is also useful to screen for nomologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr GJ;
                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                              Staphylococcus aureus cellular proliferation protein #239.
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              AAU33963 standard, protein; 309 AA
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2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
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22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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                                                                              (first entry)
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Xu HH;
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                                                                                                                                                                                                  Staphylococcus aureus.
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N-PSDB; AAS51822.
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Best Local Similarity
Matches 225; Conserv
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26-MAY-2000;
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Yamamoto RT,
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AAU33963
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                                                                                                                                                                                                                                    YSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLII 125
                                                                                                                                                            126 ADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKI 185
                                                                                                                                                                                           EEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLK 245
                                                                                              65
                                                                                                             28
of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                    6 RGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLE
                                                                                                                                                                                                                           GPYLOMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNORVDILDR
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                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                cellular proliferation protein; antibiotic;
                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                             Length 319;
                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus cellular proliferation protein #699
                                                                   8e-51;
rhes 99; Indels
                                                               DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall
                                                           Query Match 43.0%; Score 726; DB Best Local Similarity 47.1%; Pred. No. 8e-51 Matches 153; Conservative 61; Mismatches
                                                                                                                                                                                                                                                            DLWARSRGLISSEEMAKELVELSKK 328
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                                                                                                                                                                                                                                                                    AAU36529 standard; protein; 319 AA.
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; 2000US-0206848P.
; 2000US-020727P.
; 2000US-0242578P.
; 2000US-0253625P.
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                                                                                                                                                                                                                                                                                                                                                                                  prokaryotic cell
al; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
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N-PSDB; AAS54388.
                                                Sequence 319 AA;
                                                                                                                                                                                                                                                                                                                                                                                         antibacterial;
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27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
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23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                  Antisense;
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AAU36529
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coil, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, seleculation and Enterococcus facealls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins can used to screen compounds in rational drug discovery programmes. The proteins can used to acreen compounds in rational drug discovery programmes. The present equance is also useful to screen for homologous cullicate acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent celectronic format directly from WIPO at cellular proliferation in the printed specification, but was obtained in celectronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPYLOMNTETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNORVDILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLE
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   ot
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New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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47.1%; Pred. No. 8e-51;
tive 61; Mismatches 99; Indels
                                                                                                  Example 3; SEQ ID NO 12122; 511pp; English.
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Matches 153; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 319 AA;
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ABJ19052
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Tue Sep

ABU16209 standard; protein; 319 AA

ABU16209

ABU16209

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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma pool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-immunity. The hyperimmune serum-reactive antigens comprising any of the 62 sequences of 53-2261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a parameteutical preparation, against 8. aureus or 8. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament of preparation of antibodies is useful for the manufacture of a medicament of cor treating or preventing staphylococcal infections or colonisation against 8. aureus or 8. epidermidis. The autibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoimmune diseases or infections caused by viral (e.g. Hut), hepatitis A, B or C), fungal or protozoan pathogens. This advance represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 KIKSELSKIAPTIMLVSGTGDYNANIEAFKTVAKAVGKEKEGEKRLEKHDKILAEIRKKI 183
                                                                                                                                                                                                                                                                                                                                             Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 NEELANINPKVMILATDGKTDKORTKF----IDPAVWKSLKAVKDNKVYDVDRNKMLKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VVFMLILVVAVAGGGQKDT----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
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                                                                                                                                                                                                                 Zauner W;
Hafner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 319;
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                                                                                                                                                                                                               Klade C, Henics T,
ryla A, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 724.5;
46.9%; Pred. No. 1.1e
iive 63; Mismatches
                                                                                                                                                                                                                                   Dryla A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Page 212; 252pp; English.
                                                                                                                                                                      (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
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O, Etz H, I
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                                                                                   21-JAN-2002; 2002WO-EP000546.
                                                                                                                              26-JAN-2001; 2001AT-00000130.
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Matches 149, Conservative
                                                                                                                                                                                                               Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
Tempelmaier B;
                                                                                                                                                                                                                                                                                                     WPI; 2003-075410/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 319 AA;
WO200259148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 preparation.
                                          01-AUG-2002
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the 6213 antiesnes sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid conditions and inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular crowding the polypeptide; (6) inhibiting cellular crowding the polypeptide; (7) indentifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, activity; (11) a culture comprising strains in which the extent confouct is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of confounts; or (13) identifying the target of a compound that inhibits the confound confourt is overexpressed or underexpressed; (12) determining the extent confounts; or (13) identifying the target of a compound that inhibits collection of confounts. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for the provery properame or for searching in antisense uncleic acids required for collidar and provery properame or for candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                               Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or e
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                  Protein encoded by Prokaryotic essential gene #1736.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 44133; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-GOT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0362699P.
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                                                                     19-JUN-2003 (first entry)
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                                                                                                                                                                                                                 Staphylococcus aureus.
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Trawick JD,
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N-PSDB; ACA20079.
                                                                                                                                                                                                                                                              WO200277183-A2.
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Wall
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patient. They are also useful for topical disinfection in an animal mammal e.g. human. The current sequence represents an SBIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR41867 standard; protein; 325 AA
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                                                                                                                                  Query Match
Best Local Similarity 46.9%
Matches 149; Conservative
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N-PSDB; ACC48534.
                                                                                           Sequence 325 AA;
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                                                invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEIP; surface exposed immunogenic polypeptide; iron-binding; receptor; antibacterial; fungicide; protozoacide; infection; disinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Pharmaceutical compositions based on the polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 NEELANINPKVMILATDGKTDKNTTKF----IDPAVWKSLKAVKDNKVYDVDRNKMLKSR
                                                                                                                                                                  |: :| :::| | || || : ----EEKTEMTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                              73 VALDVKPVGIADDNKKORIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                                                                                              124 KIKSELSKIAPTIMLVSGTGDYNANIEAFKTVAKAVGKEKEGEKRLEKHDKILAEIRKKI
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                                                                                                                                         13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                     GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                       TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                Gaps
                                                                                                11;
                                                  Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exposed immunogenic polypeptide (SEIP) # SEQ ID 21.
                                                                                                Indels
                                                    DB 6;
                                                    42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
                                                                                                63; Mismatches
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                                                                                                Conservative
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                                                                    Local Similarity
es 149; Conserv
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             Sequence 319
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                                                      Query Match
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Matches
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                                                                                                                  72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a novel Staphylococcus aureus surface-exposed immunogenic polypeptide (SEIP). To isolate SEIP genes, an
                                                                                                                                                                                                                               73 VALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADNNRHK
                                                                                                                                                                                                                                                                : ::|| : : | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | | : : | | | EQSTLKSAFAFGISRAGMFINNEDTFMGQFLIKMGIQPEVTKDKTTHVGERKGGPYIXLN
                                                                                                               13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                                                            133 GIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
                                                                                                                                                                    15 VVFMLILVVAVAGCGQKDT----EEKTEMTTIKDELGTEKIKKNPKRVVVLEYSFADYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcal surface-exposed immunogenic polypeptide D2 SA05.
Length 325,
                                                          Indels
     DB 6;
  42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
ive 63; Mismatches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
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antieera. DNA was isolated from clones expressing SEIPs, and amino acid sequences were deduced and analysed for conserved and/or functional domains. The present SEIP has sequence homology with the siderophore family of periphasmic binding proteins. The invention provides methods for the identification, production and recovery of SEIPs. The SEIPs can be used individually, or in combination, to produce anti-staphylococal antibodies useful in passive or active immunisation strategies to prevent or contain staphylococcal infection. They can also be used to develop
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expression library of S. aureus genomic DNA was screened with anti-SEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::||:::|| :::|| | :::|| EQSTLKSAPAFGISRAGMFINNEDTFWGQPLIKMGIQPEVTKDKTTHVGERKGGPYIXLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 NEELANINFKVMILATDGKTDKNTTKF----IDPAVWKSLKAVKDNKVYDVDRNKWLKSR
                                                                                                                                                                                                                                                      VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Staphylococcus aureus protein, useful as a vaccine for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial, vaccine; gene therapy, infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                         11,
                                                                                                                                                                                           Length 325;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                          95;
                                                                                                                                                                                           42.9%; Score 724.5; DB 6
46.9%; Pred. No. 1.1e-50;
                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM72855 standard; protein; 325
                                                                                                                                                                                                                         63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|:|| ||::| ::::|
GIIASESMAEDLEKIAEK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-IB002637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                          Conservative
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N-PSDB; ACF74415.
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                                                                                                                                                                                                           Similarity
                                                                                                                                  diagnostic assays
                                                                                                                                                                 Sequence 325 AA;
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                                                                    The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
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190 EQSTLKSAFAFGISRAGMFINNEDTFWGQFLIKWGIQPEVTKDKTTHVGERKGGFYIYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETLSQVNPERMFIMTN-KASSNEPSLKELEKDP-VWKKLNAVKNQRVDILDRDLWARSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMN
preventing Staphylococcal infection, specifically an infection caused
                                                                                                                                                                                                                                                                                                                               13 VIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDAL
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                      Length 325;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #28894
                                                                                                                                                                                                                                                                      42.9%; Score 724.5; DB 6; larity 46.9%; Pred. No. 1.1e-50; Conservative 63; Mismatches 95;
                                                                                                                                                                                                           the novel S. aureus proteins of the invention
                                              Claim 1; SEQ ID NO 4190; 49pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU43367 standard; protein; 175
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GIIASESMAEDLEKIAEK 323
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06-SEP-2001, 2001US-00948933.
25-0CT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                  . aureus, e.g. sepsis
                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                            Sequence 325
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                                                                                                                                                                                                                                                                                       Local Simines 149;
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                                                                                                                                                                                                                                                                         Query Match
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ABU43367
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Pasteurella multocida.

WO200277183-A2 03-OCT-2002 21-MAR-2002; 2002WO-US009107

Protein encoded by Prokaryotic essential gene #24493

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the invention transes by an isolated in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide apolypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for the proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for repulse for cellular proliferation or the biological pathway is a gene required for cellular proliferation or the biological pathway is a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic acids are useful for strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for centifying proteins or screening for homologous nucleic acids activity in a proliferation in cells other than S. aureus, S. typhimurium, K. Dienungiae or P. aeruginosa. The present sequence is encoded by one of required form part of the printed specification, but was obtained for this or the printed specification, but was obtained for this properation of the printed specification, but was obtained for this properation of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any
                                                                                                Ohlsen KL,
Forsyth RA,
                                                                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 71291; 1766pp; English.
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                                                                                                Malone C,
Carr GJ,
(ELIT-) ELITRA PHARM INC
                                                                                           Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                         2003-029926/02
                                                                                                                                                                                                                                                                                       N-PSDB; ACA47237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                           Wang L,
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38.1%; Score 644; DB 6; Length 175; 70.9%; Pred. No. 1.8e-44; ive 23; Mismatches 24; Indels Best Local Similarity 70.98 Matches 124; Conservative Sequence 175 AA; Query Match 

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WVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEBISKLK 120 61

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ò 음 ò 121 121

ABU38966 standard; protein; 298 AA. ABU38966; RESULT 17 ABU38966 

(first entry)

19-JUN-2003

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the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

cof the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

concing a polypeptide whose expression is inhibited by the antisense

concleic acid; (2) a host cell containing the vector; (3) an isolated

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide, (5) producing the polypeptide; (6) inhibiting cellular

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the acity against a biological pathway

contiferation or that has an activity against a biological pathway

contiferation; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

confound agene required for cellular proliferation of an

confound activity; (1) a culture comprising strains in which the estent

compound activity; (1) a culture comprising strains in which the gene

confound activity; (1) a culture comprising strains in which the gene

confound sectivity; (1) a culture comprising strains in which the gene

confount is overexpressed or underexpressed; (12) determining the extent

confounts; or (13) identifying the target of a compound that inhibits the

confounts; or (13) identifying the target of a compound that inhibits

confounts; or (13) identifying the target of a compound that inhibits

confounts; or (13) identifying the target of a compound that inhibits

confounts; or (13) identifying the target of a compound that inhibits

confounts or (13) identifying the target of a compound that inhibits

confounts; or (13) identifying the targe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Will from Will at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 VEIKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 66890; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-029926/02
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proteins from Photorhabdus luminescens. The isolated sequences are correcting from Photorhabdus luminescens. The isolated sequences are sources of probles and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the CO Pypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. Combinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The antibacterials vectors containing the genes and Ab are also useful charapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as
                                            143 KIGDLIGKSKEMQARIAKHKODIADIAK--TLPKGKKAIIGVSRETOFNLYNSESYAGGL 200
                                                                                                                                                                                                                                                                                         LSQLGFK--EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKE 280
                                                                                                                                                                                                                                                                                                                                      TSVGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial, fungicide, insecticide, polymorphism, genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
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                                                                                                                                              TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LEKDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVELSKKDSK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 WENEALWKIIPAVKNGQVILANDNLWARARGIDAAEVWAKEVQDFVTKSAK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kunst F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photorhabdus luminescens protein sequence #1451.
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(CNRS ) CNRS CENT NAT RECH SCI
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                                                                                                                                                                                                                                                                                                                                        223 LSQLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELE 282
                                                                                                                                                                                                                                                                                                                                                           202 LTALGLKVPASVN------HAAMVSLNLEQLIALNPDWLIVAHYR---QESIVKRWQ 249
biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                        144 IIGKVWGKESEMQKRLAEHRERMKGYASQ--LPQGVSVVFGTSREQQFNLHSSDTYTGSV
                                                                                                                                                               43 VEIKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKY
                                                                                                                                                                            24 VIVQDEQGSFILMTVPQRVVVLELSFADALAAINISPVGIADDNDPQRILIDVRQRIKFW
                                                                                                                                                                                                                                                                                 163 TISKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQF
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                                                                                                                                   Gaps
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                    Ouery Match 28.2%; Score 476; DB 6; Length 303; Best Local Similarity 36.0%; Pred. No. 2e-30; Matches 102; Conservative 60; Mismatches 107; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                  283 KDPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
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Forsyth |
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 56054; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU28130 standard; protein; 300
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Trawick JD, Carr GJ,
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25-OCT-2001; 2001US-0342923P.
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06-MAR-2002; 2002US-0362699P
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                                                                          Sequence 303 AA;
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WO200170955-A2.

27-SEP-2001

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, or that has an activity against a biological pathway confideration, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antiblocit; (10) profiling a compound; sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of product is overexpressed or underexpressed; (12) determining the extent of compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational correctivity proventy programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. patent did not forme part of the printed specification, but was obtained to the print of the printed specification, but was obtained to the printed specification, but we obtained to the printed specification, the printed specification, the printed specification, the printed specification of the printed speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 35.85
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 300 AA;
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164 84 VGTRAQPSLEAIAALKPDLIIADSSRHAGIYTALQQIAPVLLLKSRNETYAENLHSAAII 143 45 IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 104 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS 224 OLGFKEALSDDVTKGLSKYLKGPYL-QMNTETLSQVNPERMFIMTNKASSNEPSLKELEK 283 83 24 VQDEHGTFTLDKTPQRIVVLELSPADALAAVDVSPIGIADDNDAKRILPEVRAHLKPWQS VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI 249 DPLWQILTAAQKQQVASVDSNAWARMRGIFAAERIAADTVKI 290 284 DPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVEL 325 105 셤 ઠે 셤 ሯ 셤 ò 셤 ઠે 셤

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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                       E. coli cellular proliferation protein #457.
AAU34876 standard; protein; 302 AA
                                                 (first entry)
                                                                                                                                    Escherichia coli
                                                 14-FEB-2002
                         AAU34876;
   X S X & X E X E X B X S X B
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonala typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also casful for the identification of potential new targets for antibiotic proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antibodies capable of binding to the expressed proteins. The present compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 VQDEHGTFTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS
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                                                                                                                                                                                                                                                                             Carr
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                                                                                                                                                                                                                                                                             Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.2%; Score 460; DB 4; Length 302; 35.5%; Pred. No. 4e-29; ive 62; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|: | : |:| : |:| | DPLWQMLTAAQKQQVASVDSNTWARMRGIFAAERIAADTVKI 292
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                                                                                                                                                                                                                                                                           Wall
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                                                                                                                                                                                                                                                                             Zyskind JW,
                                                                                                                  2000US-0206848P.
2000US-0207727P.
                                                                                                                                                   23-0CT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
                                                                 21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                             Ohlsen KL,
Xu HH;
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                                                                                                                                                                                                                                            ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                WPI; 2001-611495/70.
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                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS52735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 302 AA;
                                                                                                                                                                                                                                                                             Haselbeck R,
                                                                                                                                                                                                                                                                                                 Yamamoto RT,
                                                                                                                                      26-MAY-2000;
                                                                                                                        23-MAY-2000;
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The invantion relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
outleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation or the activity of a gene in an operon required for
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the strains
compound's activity; (11) a culture comprising strains in which the strains
compound's activity; (12) determining the extent
compound's or intifying the target of a compound that inhibits the
compound's proliferation of an organism. The antisense nucleic acids required
confideration of an organism. The antisense nucleic acids required
dence of the definity and proliferation or for solate encladidate molecules for rational
dence of the dence of the strains is present in a culture or collection of
confideration of an organism. The antisense mucleic acids required
confideration of an organism. The antisense confideration of an organism.
The antisense and definity maniformed acids required
confideration of an organism of the strains of the strains of the strains of the strains of the strains of the strains of the strains of the str
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #14408
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Yamamoto R,
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                                          ABU28881 standard; protein; 302 AA
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                          (first entry)
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Trawick JD,
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                                                                                                                                    ABU28881;
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ABU2888:
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203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the
                                                                                       85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                             GEMVGKKREMQARLEQHKERMAQWASQ--LPKGTRVAFGTSREQOFNLHTQETWTGSVLA
                                                                                                                                     86 VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII
                                                                                                                                                                                                                                         225 OLGFKEALSDDVTKGLSKYLKGPYL-OMNTETLSQVNPERMFIMTNKASSNEPSLKELEK
                                                         45 IKHEEGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                             105 VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIBLKSFDGDYNENIDAFKTI
                                                                                                                                                                              165 SKALGKEBEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                               16;
27.2%; Score 460; DB 6; Length 302; 35.5%; Pred. No. 4e-29;
                             Indels
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                                                                                                                                                                                                                                                                                                  284 DPVWKKLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                                                                                                                                                   Ohlsen Porsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #27023.
                           62; Mismatches 104;
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                           ABU41496 standard; protein; 297
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Query Match
Best Local Similarity 35.5%
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas syringae.
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Trawick JD,
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Wall
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continued and the polypeptide; (6) inhibiting cellular prolypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicitic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene product is overapressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational conditions or screening for homologous nucleic acids required for proliferation in cells other than S. S. typhimurium, c. M. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 LDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRHKGI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 YKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEEYKKEITM 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKNOKYLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQMNTE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 TLSQVNPERMFIMTNK----ASSNEPSLKEL-EKDPVWKKLNAVKNQRVDILDRDLWARS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 LFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKV--PKHPKRVVVLEYSFVDALVA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------QAAPIDIDDĞQHKVHLPDTPKRVVVLEPSFLDGLAS 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.9%; Score 454; DB 6; Length 29
34.3%; Pred. No. 1.2e-28;
ive 60; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus protein SEQ ID #5193.
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Matches 109; Conservative
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This sequence represents a Staphylococcus aureus protein sequence of the invention. The DNA sequences encoding the S.aureus proteins are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.

Co disk, random access memory (RAM), read-only memory (ROM) or CD-ROM.

Co functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained.

Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a waccine composition cagainst S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food consoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the Shin syndrome, toxic shock syndrome, etc. Organisms transformed with the CD DNA sequences can be used for recombinant production of the polypeptides.

CC DNA sequences can be used for recombinant production of the polypeptides.

CC DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the 5191 S.aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKYLKG--PYLOMNT-ETLSOVNPERMFIMTNKASSNEPSL----KELEKDPVWKKINA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGOFLSOLGFKEALSDDVTKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQK-----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAĞEILNDLGFKR-----NKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                              Ŝ
                                                                                                                                                                                                 Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.0%; Score 405; DB 2; Length 330; 32.8%; Pred. No. 1.4e-24; ive 65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                              Fannon MR,
                                                                                                                                                                                              Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                              Claim 23; Page 3189-3190; 3271pp; English.
                                                                                                                                                                                              Barash SC,
                                                                           97EP-00100117
                                                                                                                   96US-0009861P
                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 32.89
Matches 113; Conservative
                                                                                                                                                                                                                                      WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                        S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 330 AA;
                                                                                                                   05-JAN-1996;
                                                                             07-JAN-1997;
EP786519-A2
                                     30-JUL-1997
                                                                                                                                                                                                 Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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AAY42331 standard; protein; 330 AA.

RESULT 24 AAY42331 ID AAY

Staphylococcus aureus.

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241 SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                             179 FQK----DAKAKYKDAWPLKASVVNFRADHTRIYAGGYAGEILNDLGFKR-----NKDL
         YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL
                                                                                                                     293 VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                    "antigenic epitope-bearing region"
                                                                                                                                                                                                                                                                                                                           CbrA; infection; therapy; diagnosis; vaccine; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "antigenic epitope-bearing region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "antigenic epitope-bearing region"
                                                                                                                                                                                                                                                                                                Staphylococcus aureus iron regulation protein cbrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      733. .236
/note= "antigenic epitope-bearing
243. .247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "antigenic epitope-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "antigenic epitope-bearing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope-bearing
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                .54
.se= "antigenic e
                                                                                                                                                                                                                  AAY31824 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 25; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
(LUDW-) LUDWIG INST CANCER RES
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98US-0080296P.
98US-0084674P.
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                                                                                                                                                                                                                                                                        06-DEC-1999 (first entry)
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choi GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-562101/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ19889.
                                                                                                                                                                                                                                                                                                                                          iron regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson AJG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1998;
07-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections.
                                                                                                                                                                                                                                             AAY31824;
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Region
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                                                                                                                                                                                          RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents Staphylococcus aureus cbrA protein. The cbrA protein is predicted to have a molecular weight of about 36.8 kD and, along with cbra (AAY42332) and cbrC (AAY42333), is thought to be involved in iron regulation, based on amino acid sequence homology with known iron regulator proteins. S. aureus is a ubiquitous pathogen which causes infections, neonatal conjunctivitis, evelid infections, food poisoning, joint infections, neonatal conjunctivitis, osteomyelitis, skin infections, carteus is increasingly becoming resistant to known antibiotics, with methicillin-resistant strains generally being multiply drug resistant. Methicillin-resistant S. aureus (MRGA) poses serious infection control problems, with many strains being multiresistant against virtually all antibiotics with the exception of the vancomycin-type glycopeptide antibiotics. The protein may be useful to screen potential antagonists with could be used as antibiotics and it may be used as a vaccine to prevent or attenuate an infection caused by a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus genus. The protein, or antibodies against it can be used in immunoassays to detect Staphylococcus in a biological sample. Probes and primers derived from the nucleic acid sequences may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%; Score 405; DB 2; Length 330;
32.8%; Pred. No. 1.4e-24;
ive 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus genes and polypeptides, vectors and methods of
                                                                                           Infection; detection; diagnosis; screening; antibiotic; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect Staphylococcus nucleic acids in a biological sample
                                                                  Staphylococcus aureus cbrA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 25; 111pp; English.
                                                                                                                                                                                                                                                                                                 HUMAN GENOME SCI INC.
LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                           98US-0078682P.
98US-0080296P.
98US-0084674P.
                                                                                                                                                                                                                   99WO-US006199.
                                       (first entry)
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Best Local Similarity 32.81
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant production
                                                                                                                                                                                                                                                                                                                                          Choi GH;
                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-580304/49.
                                                                                                           methicillin; MRSA.
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ22850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 330 AA;
                                                                                                                                                                                                                                                                                                                                          Simpson AJG,
                                                                                                                                                              WO9947662-A1.
                                                                                                                                                                                                                     L8-MAR-1999;
                                                                                                                                                                                                                                              20-MAR-1998;
                                       20-DEC-1999
                                                                                                                                                                                                                                                           01-APR-1998;
07-MAY-1998;
                                                                                                                                                                                          23-SEP-1999,
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              AAY42331
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region" region"

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New isolated Staphylococcus nucleic acid molecules, used to develop products for the diagnosis, prevention and treatment of Staphylococcal
                                                                                                                                                                                                                                                                                                                                                     This is the deduced sequence of the novel 36.8 kDa cbrA protein of Staphylococcus aureus strain ISP3 (ATCC 202108), as predicted from
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12;
           homology to known proteins involved in iron regulation. The invention provides 11 novel genes (see AAZ19882-92) of S. aureus and the provides 11 novel genes (see AAZ19882-92) of S. aureus and the host cells, antibodies and hybridomas. The invention further relates to screening methods for identifying agonists and antagonists of S. aureus polypeptide activity, and to diagnostic methods for detecting staphylococcus nucleic acids, polypeptides and antibodies in a biological sample. Antagonists of cbrA may be useful as antibiotics to treat infections of S. aureus and other Staphylococcus spp. Also provided are novel vaccines for the prevention or attenuation of infection by Staphylococcus. CbrA polypeptides can also be used to detect S. aureus in immunoassays, as epitope tags, mol.wt. markers, to raise antibodies and as vaccines against S. aureus and other Staphylococcus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SKYLKG--PYLOMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGKKRLEEHDKKIEE 187
                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                        8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV; hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer; autoimmune disease; HIV; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pathogen specific antigen related staphylococcal protein SEQ ID No 346.
                                                                                                                                                                                                                                                                                                                                                                                                CbrA shows amino acid sequence
                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                   24.0%; Score 405; DB 2; Length 330; 32.8%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKNQRV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                       65; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
genomic DNA (see AAZ19889).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2002; 2002WO-EP000546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-2001; 2001AT-00000130
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                                                                                                                                                                                                                                                                                                       Query Match 24.0
Best Local Similarity 32.8
Matches 113; Conservative
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                                                                                                                                                                                                                                                                    Sequence 330 AA
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The invention relates to a novel method for identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, tumour, allergen, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma cool of a type of animal, or individual sera with antibodies against the pool of a type of animal, or individual sera with antibodies against the specific pathogen, tumour, allergen, tissue or host prone to auto-cimmunity. The hyperimmune serum-reactive antigens comprising any of the sequences of 53-2261 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a pharmaceutical preparation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The preparation of antibodies is useful for the manufacture of a medicament or against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be treated include cancer, autoinmune diseases or infections caused by viral (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This sequence represents a staphylococcal protein relating to the method for identifying and producing pathogen specific antigens of the invention
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   Zauner Wa
Hafner N
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C, Henics T,
Weichhart T,
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   u, Klade C
, Dryla A,
                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 214; 252pp; English.
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   Von Ahsen U,
O, Etz H,
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          Meinke A, Nagy E, Von
Minh DB, Vytvytska O,
                                                                                                                                              WPI; 2003-075410/07.
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Novel surface-exposed immunogenic polypeptide of Staphylococcus aureus containing receptors for siderophores or iron-binding ligands, useful for producing antibodies effective against Staphylococci infection.
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                                                                                                                                                                Surface-exposed immunogenic polypeptide; SEIP; siderophore; receptor;
                                                                                                Staphylococcal surface-exposed immunogenic polypeptide D2 SA02.
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                            11-AUG-2003 (first entry)
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                                                                                                                                                                                                       antibacterial; vaccine
                                                                                                                                                                                                                                                                       Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OKOVDNGKDIIOLISKESIPLMNADHIFVVKSDPNAKDAALVKKTESEWISSKEWKNLDA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolating microbial target surface exposed immunogenic polypeptides, by immunizing host with microbial membrane-associated polypeptides to produce antibodies and using antibodies to isolate target polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the isolation of target surface exposed immunogenic polypeptides (SEIP) from microorganisms. The SEIP's of the invention are receptors of iron-binding molecules. The activity of polypeptides of the invention may be described as antibacterial, fungicide and protozoacide. Pharmaceutical compositions based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides of the invention are useful for treating infections and diseases caused by microbes including bacteria, fungi and protozoa in epatient. They are also useful for topical disinfection in an animal or mammal e.g. human. The current sequence represents an SEIP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
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                            SEIP; surface exposed immunogenic polypeptide; iron-binding; recantibacterial; fungicide; protozoacide; infection; disinfection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.0%; Score 405; DB 6; Length 33 32.8%; Pred. No. 1.4e-24; rive 65; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DSQU-) D-SQUARED BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 40; 46pp; English.
                                                                                                                                                                                                                                                                                                                                        10-JUL-2002; 2002WO-US021663.
                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2001; 2001US-0304390P
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Best Local Similarity
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                                                                                                                                                                                                    WO2003006672-A2
                                                                                                                                                                                                                                                                       23-JAN-2003
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Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scott DL;
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Length 330;

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Malone C,
Carr GJ,
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06-SBP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis.
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                                                                                                                                                                                                                                                                                                                                                                                   WO200277183-A2.
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179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a new isolated nucleic acid molecule comprising: a sequence that is 91% identical to a fully defined sequence having 586-226 bp, or its complement; or a sequence encoding a polypeptide having a fully defined sequence comprising 136-691 amino acids, or its complement. The gene is Staphylococcus aureus gene. The nucleic acid is useful for preparing a vaccine against infection caused by Staphylococcus aureus. The methods are useful for preventing or attenuating an infection caused by a Staphylococcus, detecting Staphylococcus nucleic acids in a biological sample obtained from an animal, and detecting Staphylococcus auritobodies in a biological sample obtained from an animal. This is the amino acid sequence of Staphylococcus aureus cbrA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEPAPNLEEISKLKPDLIVAS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIAD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 YKKEITMDKNQKVLPAVAAKSGLLAHPSN-----SYVGQFLSQLGFKEALSDDVTKGL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus gene, useful for preparing a vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 NNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LKILSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
24.0%; Score 405; DB 7; Length 330;
Best Local Similarity 32.8%; Pred. No. 1.4e-24;
Matches 113; Conservative 65; Mismatches 132; Indels 34; Gaps
                                                                                                                                                                    antibacterial; immunostimulant; vaccine; vaccine;
Staphylococcus aureus infection; infection prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection caused by Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 16; 61pp; English.
                                              ADF43556 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                      98US-0078862P.
98US-0080296P.
98US-0084674P.
99WO-US006199.
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                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2002; 2002US-00830217
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                   infection attenuation; cbrA
                                                                                                                                        Staphylococcus aureus cbrA
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi GH;
                                                                                                                                                                                                                                 Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-897737/82.
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01-APR-1998;
07-MAY-1998;
18-MAR-1999;
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                                                                                                        12-FEB-2004
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                                                                           ADF43556;
                 RESULT 29
                                ADF43556
ID ADF
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concluded are: (2) a host cell containing the vector; (3) an isolated cucleic acid; (2) a host cell containing the vector; (3) an isolated contisense nucleic acid; (4) an antibody capable of specifically binding cartisphenica; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for conjudence or the farm an activity against a biological pathway required for proliferation, or that has an activity against a biological pathway in which a proliferation or the biological pathway in which a proliferation required gene or the biological conspund's activity; (11) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a congound's activity; (11) a culture comprising strains in which the gene congration of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                           228
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                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
SKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL----KELEKDPVWKKLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                            293 VKNORV-DILDRDLWARSRGLISSEEMAKELVELSKKDSKKDNK 335
                                                                                                                                                                                                                                                                                                                                            289 VKNNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQSK 330
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Forsyth |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 45599; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU17675 standard; protein; 324 AA.
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EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
         identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                               EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKQPNLEBISKLK 120
                                                                                                                                                                                                                                                                                                                               PDLIIADNNRHKGIYKDLNKIAPTIEL---KSPDGDYNENIDAPKTISKALGKEEEGKKR 177
                                                                                                                                                                                                                                                                                                                                                                                          PDLIITASFRGKAIKNELEQIAPTVMFDPSTSNNDHFAEMTETFKQIAKAVGKEEEGKKV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                  LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KILSI----FIVVFLFAVGCGQQKEEKKETKADNKNQAITIKHAEGETKLDKPAKKVVVL 58
The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                     9 KILSVIGLLFVLIATAACGNNSSSNSSKESSKD----GVEIKHEEGTTKVPKHPKRVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                         40;
                                                                                                                                                                                        Length 324;
                                                                                                                                                                                                                       59; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
                                                                                                                                                                                           23.1%; Score 391; DB 6; 34.4%; Pred. No. 1.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #8842.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG08851 standard; protein; 1132
proliferation of an organism.
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2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                           Query Match
Best Local Similarity 34.4
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS73038
                                                                                                                                                               Sequence 324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

creation (PRX) primers, oligomers, and for chromosome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

can diagnostics as expressed sequence tags for identifying expressed

consideration gene therapy techniques to reserve normal

cativity of (II) or to treat disease states involving (II). (II) is

cuseful for generating antibodies against it, detecting or quantitating a

colypopide in fissue, as molecular weight markers and as a food

cupplympeptide in tissue, as molecular weight markers and as a food

cupplympeptide and polymucleoties sequences have applications in

characteristics, forensics, gene mapping, identification of mutations

cresponsible for genetic disorders or other trasts to assess blodiversity

cresponsible for genetic disorders or other trasts to assess blodiversity

cresponsible for genetic disorders or other trasts to assess blodiversity

can to produce other types of data and products dependent on DNA and

amino acid sequences of the invention. Note: The sequence data for this

can occupant of commat directly from WIPO at

colftp.wipo.int/pub/published_pct_sequences

colftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 VGTRAQPSLEAIAALKPDLIIADSSRHAGVYIALQQIAPVLLLKSRNETYAENLQSAAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 VQDEHGTLTLEKTPQRIVVLELSFADALAAVDVIPIGIADDNDAKRILPEVRAHLKPWQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 VGTRKQPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 SKALGKEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSNSYVGQFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 QLGFKEALSDDVTKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 SLGL-----NVPAAMAGASMPSSPGPLGASCPPRCSIHAITVTSTTPCL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --WIPGSVIRCRPVGVLKMIDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 PVWKKLNAVKNQRVDIL-----DRDLWARSRGLISSE----EMAKELVELSK 327
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations tesponsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic;
food supplement, medical imaging, diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.2%; Score 375; DB 4; Length 1132; 32.5%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Mismatches 115; Indels
                                                                                                           Claim 20; SEQ ID NO 39210; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #13139.
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Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG13148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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      X B X S X & X E X B X B X B X B
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Matches
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                                                                                                                                                                                                                                                                                     The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 IKHEEGTIKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 VGTRKOPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Score 350; DB 4;
46.6%; Pred. No. 1.7e-19;
iive 33; Mismatches 46
                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 43507; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 GEMVGKKREMQARLEQHKERMAQWASQL 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKALGKEEEGKKRLEEHDKKIEEYKKEI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM73050 standard; protein; 287
                             30-MAR-2001; 2001WO-US008631
                                                       31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 46.6%
nes 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                     WPI; 2001-639362/73
                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                    N-PSDB; AAS77335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 932 AA;
                                                                                                                                                                                                                                        biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM73050;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 QPNLEEISKLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEEEGKKRLEEHDKKIEEYKKEITMDKNOKVLPAVAAKSGLLAHPSN-----SYVGQF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSQLGFKEALSDDVTKGLSKYLKG--PYLQMNT-ETLSQVNPERMFIMTNKASSNEPSL- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KELEKDPVWKKLNAVKNQRV-DILDRDLWARSRGLISSEEMAKELVELVELSKKDSKKD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYTESEWTSSKEWKNLDAVKNQVSDDLDEITWNLAGGYKSSLKLIDDLYE--KLNIEKQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GTTEIKGKPKRVVTLYQGATDVAVSLGVKPVGAVESWTQKPKFEYIKNDLKDTKIVGQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 20.3%; Score 343; DB 6; Length 287; Local Similarity 32.1%; Pred. No. 1.4e-19; les 97; Conservative 58; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4580; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG90121 standard; protein; 315 AA
enzymatic assay; antibiotic target
                                                                                                                                                                                                                                        27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                               27-MAR-2001; 2001GB-00007661.
                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-120786/11.
N-PSDB; ACF74610.
                                                                                                                                                                                                                                                                                                                                                      (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 287 AA;
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SK 287
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 KGIYKDLMKIAPTIELKSFDGDYNENIDAFKTISKALGKEEGGKKRLEEHDKKIEBYKKE 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTETLSQVNPERMF--IMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 SSENFGQIDGDLIFYTIPGSPEATTYPKISEL-----WUDSPAVRQGRIYEFEDETWANG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 LVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQPNLEEISKLKPDLIIADNNRH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 VIGLLFVLIATAACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H; Senoh A, Ikeda M, Ozaki A;
                                                                                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                       C glutamicum protein fragment SEQ ID NO: 3875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1999; 99JP-00377484.
07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                                                                                                                                                                                                                                                        Corynebacterium glutamicum
(first entry)
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26-SEP-2001
                                                                                                                                                                                                                                                                                                                            BP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakagawa S,
Tateishi N,
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Best Local
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the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a wetoor comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits elular proliferation; (8) identifying a gene required for cellular proliferation or the sequired for cellular proliferation of the sense of pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of proliferation of an organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for information of an organism of an organism of an organism of an organism of collection of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of a compound of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurtum, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #10870.
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Yamamoto R,
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                                                                                                                                                      ABU25343 standard; protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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298 IGVLGANEILDDLEE 312
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                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium difficile
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Trawick JD,
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                                                                                                     RESULT 3
ABU25343
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                                                                                                                                                                184
                                                                                                                                      124 GRQEDFYEQLSKIAPTISTSKDDKKYLESVKNNID---KIAKIFGVEEKANQEFSKIEKK 180
                                                                                                                                                                                                     IEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEALSDDVTKGLSKYL 244
                                                                                                                                                                                                                                           245 KGPYLQMNTETLSQVNPERMFIM-----TNKASSNEPSLKELEKDPVWKKLNAVKNQRVD 299
                                                                                                                                                                                                                                                       235 HGQ--NITFEYIAKQNPEVMPVIDRGIATGSDVKESSTAKSVLNNDIIKSMDAYKNDNII 292
                                                                                    70
                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                              11 IAIIGLVTVF---ALGGSKKNESKTSENSNNTIKITHNLGETDVKLNPKKVVVFDYSALD
                                                                                                                                                               NRHKGIYKDLNKIAPTIELKSFDGDYNE----NIDAFKTISKALGKEEEGKKRLEEHDKK
                                                                                                                                                                                                                181 IETLNKKVT-DKNLNALTIMVNEGNLSVFGEESRFSILYNSFGF----ENKDKNIKESS
                                                                                    11 LSVIGLLFVLIATAACGNNSSSNSSKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVD
                                                                                                                         ALVALDVKP--VGIADDNKKNRIIKPLRDKIGKYTSVGTRKOPNLEEISKLKPDLIIADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                  30; Gaps
                                               Length 321;
                                              ; Score 327; DB 6; Length 32; Pred. No. 3.2e-18; 55; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #3886.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 46283; 1766pp; English
 in electronic format directly from WIPO at
         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                   ABU18359 standard; protein; 314 AA
                                                                                                                                                                                                                                                                                  300 ILDRDLW-ARSRGLISSEEM 318
                                                                                                                                                                                                                                                                                                    293 YLDSPTWYVNDGGLTSLNKM 312
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
                                               19.3%;
30.9%;
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                                                                  99; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ACA22229
                             Sequence 321 AA;
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25-OCT-2001;
08-FEB-2002;
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                                               Query Match
Best Local
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The involution relates to an inclusion where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense continued acid; (2) a host cell containing the vector; (3) an isolated continued in a polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular continued for that has an activity against a biological pathway contiferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8) centured for cellular proliferation or the biological pathway in which a proliferation for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound value activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling to proliferation of an organism. The antisense nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the confidentifying proliferation to isolate conditions or collection of an organism. The present sequence acids required for proliferation in cells other than S. aureus, S. typhimurium, confident file activity grown processed or prosessed or processed or processed or processed or conditions or screening for bomologous nucleic acids are useful or formed and processed or processed or conditions or screening for promolegous nucleic acids are useful or form part of the printed specification, but was obtained for provine or the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 VDALVALDVKPVGIADDNKKNRIIKPLRDKIGKYTSVGTRKQP--NLEEISKLKPDLIIA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 DNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKRLEEHDKKIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYLKGPYLOMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDIL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LKOTMAQVSLEGLVAFQPDQMFIV-NFGGEADKVYEDYKNSAVWKDNKAVKONNHVYEV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYV-GQFLSQLGFKEALSDDV----TKGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 314;
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29.9%; Pred. No. 4.3e-17;
cive 65; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNEVFNTKAFNPIGKDMLIDEIAKEILAKNK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRDLW-ARSRGLISS----EEMAKELVELSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. faecium protein sequence SEQ ID 4516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-2004
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The invention relates to an isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the for comprising 40 acquential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridishing to it). Also included are a recompliant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids are chosen from Eacle is useful for diagnosing pathological conditions resulting from E faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans addrived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcue faecium infections. The present sequence represents one of the containing the nucleic acid are useful for preventing or an efficient acid and processions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 SKLKPDLIIADNNRHKGIYKDLAKIAPTIELKSFDG-----DYNENIDAFKTISKALGKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSGLLAHPSNSYVGQFLSQLGFKEA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
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Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VRGLKILSVIGLLFVLIATAACG--NNSSSNSSKESS---KDGVEIKHEEG-TTKVPKHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKVVVPDNGSLDTMDALGVGDKVVGAATSS-----LPEVLSSYKKVESAGGIKEPDLEKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Gaps
Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%; Score 307.5; DB 7; Length 31.3%; Pred. No. 1.4e-16; ive 65; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 4516; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                     98US-00107532.
                                                                                                                                                                                                                                                                                                                                                                                     97US-0051571P.
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                                                                                                           Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-799836/75.
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                                                                                                                                                                                                                                                                                                                     30-JUN-1998;
                                                                                                                                                                            US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                24 - JUN - 2003
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the invention fracts to an instruction of a cell. Also included are:

(1) a vector comprising a product of a cell. Also included are:

(1) a vector comprising a product operation of a cell. Also included are:

(1) a vector comprising a product operation of a cell. Also included are:

(2) a vector comprision and a cell containing the vector;

(3) an isolated

(4) a net cell containing the vector;

(5) a host cell containing the vector;

(6) inhibited by the antisense

(7) identifying a compound that influences the activity of

proliferation or the activity of a gene in an operon required for

proliferation, (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

required for proliferation, or that inhibits proliferation of the biological

centrifying a gene required for cellular proliferation of the biological

centrifying a gene required for cellular proliferation of an

corganism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (11) a culture comprising strains in which the gene

compound's activity; (12) a culture comprising strains in which the gene

compound's activity; (12) a culture comprising strains in which the gene

compound's activity; (13) a culture comprising strains in which the gene

compound's activity; (13) a culture comprising strains in which the gene

compound's activity; (13) a culture compound that inhibits the

compound's activity of (13) identifying the farget of a compound that inhibits the

compound's activity of (13) identifying the carget of a compound that inhibits the

compound's activity of the strains in the activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one of
                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
287 WKKINAVKNORVDILDRDLWARSRGLISSEBMAKELVELSKK 328
                            311 VAÇTINAÇKNQQIISLEPDVWYLSGGGLESMKLMIEDVNQAFK 352
                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #2988
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                                                                                                                                                                          ABU17461 standard; protein; 314
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25-007-2001; 2001US-0342923P.
08-PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis.
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                                                                                                                                                                                                                            ABU17461;
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Matches
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                                                                                                                                                                                                                                              FKOYD-------EKASKIHDKIVAKTGDAKFMKMAAYP-NAF--RVYGDYGYGSV 216
                                                                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                             -----KKNRIIKPL----RDKIGKYTSVGTRKQPNLEEIS 117
                                                                                                                                                                                     KLKPDLIIADNNRHKGIYKDLNKIAPTIELKSFDGDYNENIDAFKTISKALGKEEEGKKR 177
                                                                                                                                                                                                  AAKPDLILV-NNRQEKIYDQLSKIAPTVMLKT---PLDQWRPKFEEVGQIFGKEKTKEW 171
                                                                                                                                                                                                                           LEEHDKKIEBYKKEITMDKNQKVLPAVAAKSG-----LLAHPSNSYVGQFLSQLGFKEA 231
                                                                                                        70
the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                    16 LLFVLIAT----AACGNNSSSNS-SKESSKDGVEIKHEEGTTKVPKHPKRVVVLEYSFVD
                                                                                                                                                                                                                                                                  LSDDV----TKGLSKYLKGPYLQMNTETLSQVNPERMFIMTNKASSNEPSLKELEKDPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW;
Xu HH;
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                     16;
                                                                  17.8%; Score 301; DB 6; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen KL,
Forsyth RA,
                                                                                      106; Indels
                                                                                                                                                                                                                                                                                                         KKLNAVKNQRVDILDRDLWARSRGLISSEEMAKELVELSKK 328
                                                                                                                                                                                                                                                                                                                            KOMNAVKNNHV------FTIKNEELNKGYFPLGKE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein encoded by Prokaryotic essential gene #3796.
                                                                            Pred. No. 4.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto R,
                                                                                       66; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             ABU18269 standard; protein; 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-00948993.
2001US-0342923P.
2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-00815242
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                                                                                                                                                 ALVALDVKPVGIADDN---
                                                                             27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                       93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus anthracis
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ACA22139
                                                 Sequence 314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2001; 25-OCT-2001; 208-FEB-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001;
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                                                                  Query Match
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Matches 9
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Wall
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the invention relates to an isolated nucleic acid comprising any one of the fell antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded by the antisense antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or that has an acityly agency of the gene product or that has an acityly agency required for proliferation or that has an acityly agency required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (13) identifying the target of a compound that inhibits proliferation of an organism. The antisense nucleic acids required for cellular proliferation in cells of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. and in the target profarms, or for screening honologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. the target prokaryotic essential genes. Note: The sequence is encoded by one of the target prokaryotic format directly from NIPO at entired sequence is encoded by one of the prince of the prince of appendication, but was obtained to the control of the prince of appendication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEHDKKIEEYKKEI----TMDKNQKVLPAVAAKS----GLLAHPSNSYVGQFLSQLGFK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EALSDDVTKGLSKYLKGPYLQMNTETLSQVNPER-MFIMTNKASSNEPSLKELEKDPVWK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LADMDKAFADAKAKIEKADLKDKNIAMAQAFTAKNVPTFRILT--DNSLALQVTKKLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYSFVDALVALDVKPVGIADDNKKNRII----KPLRDKIGKYTSVGTRKQPNLEEISKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLIIADNNRHKGIYKOLNKIAPTIEL---KSFDGDYNENIDAFKTISKALGKEBEGKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.8%; Score 300; DB 6; Length 264;
33.6%; Pred. No. 4e-16;
tive 50; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKFKKENKMYNLKGDTWIFG-GPESATSLATQVADV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLNAVKNORVDILDRDLWARSRGLISSEEMAKELVEL 325
SEQ ID NO 46193; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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ABN90518 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37560. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DKKKISNITVEVPKNPKNAVVLDYGALDVL----KELGVADKVKGLPKGENNQSLPKFLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 NENI -- DAFK---TISKALGKEREGKKRLEEHDKKIEEYKKEITMDKNQKVLPAVAAKSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 LSTFGPGGRFGGLVFDTLGFKPA------DKKVSKSPHGQNINNEYINKQNPDVILAM 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 LLAH-PSNSYVGQFLSQLGFKEALSDDVTKGLSKYLKGPYLQ-MNTFTLSQVNP---- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 ERMFIMTNKASSNEPSLKELEKDPVWKKLNAVKNQRVDILDRDLWARSRGLISSEEMAKE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KIGKYTSVGTRKOPNLEEISKLKPDLI-IADNNRHKGIYKDLNKIAPTIELKSFDGDY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GVESVRGLKILSVIGLLFVLIATAACGNNSSSNSSKES-SKDGVEIKHE-------48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 -----EGTTKVPKHPKRVVVLEYSFVDALVALDVKPVGIADDNK-----KNRIIKPLRD 97
                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.5%; Score 296.5; DB 5; Length 351; 28.4%; Pred. No. 1.1e-15; tive 70; Mismatches 131; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 5492; 267pp; English
                                                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                          97US-0055779P.
                                                                                                                            98US-00134001
antibacterial; gene therapy
                                                                                                                                                                                                                                         Doucette-Stamm LA, Bush D;
                               Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.4%
Matches 104, Conservative
                                                                                                                                                                                                                                                                       WPI; 2002-381255/41.
N-PSDB; ABN93192.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 351 AA;
                                                               JS6380370-B1
                                                                                                                              3-AUG-1998;
                                                                                                                                                           14-AUG-1997;
08-NOV-1997;
                                                                                            30-APR-2002.
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Search completed: August 25, 2005, 09:26:45 Job time : 172 secs